

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 10:47:22 ; Search time 37 Seconds
(without alignments)
2044.812 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2036
Sequence: 1 MGLWALLPGWVSATLLALLA.....WCCHVSCRNCTHTRVLHECL 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	2036	100.0	370	12	US-10-285-976-1	Sequence 1, Appli
2	906	44.5	352	12	US-10-028-248A-71	Sequence 71, Appl
3	843.5	41.4	352	12	US-09-954-342-34	Sequence 34, Appl
4	840.5	41.3	355	12	US-10-285-976-7	Sequence 7, Appli
5	840.5	41.3	355	12	US-09-954-342-36	Sequence 36, Appl
6	840	41.3	351	10	US-09-978-295A-226	Sequence 226, App
7	840	41.3	351	10	US-09-978-697-226	Sequence 226, App
8	840	41.3	351	10	US-09-978-192A-226	Sequence 226, App
9	840	41.3	351	10	US-09-999-832A-226	Sequence 226, App
10	840	41.3	351	11	US-09-978-189-226	Sequence 226, App
11	840	41.3	351	11	US-09-978-608A-226	Sequence 226, App
12	840	41.3	351	11	US-09-978-585A-226	Sequence 226, App
13	840	41.3	351	11	US-09-978-191A-226	Sequence 226, App
14	840	41.3	351	11	US-09-978-403A-226	Sequence 226, App
15	840	41.3	351	11	US-09-978-564A-226	Sequence 226, App
16	840	41.3	351	11	US-09-999-833A-226	Sequence 226, App
17	840	41.3	351	11	US-09-981-915A-226	Sequence 226, App
18	840	41.3	351	11	US-09-978-824-226	Sequence 226, App
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30	840	41.3	351	12	US-10-002-967A-226	Sequence 226, App
31	840	41.3	351	12	US-10-017-083A-226	Sequence 226, App
32	840	41.3	351	12	US-10-143-030A-226	Sequence 226, App
33	840	41.3	351	12	US-10-199-672-80	Sequence 80, Appl
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35	840	41.3	351	12	US-10-194-457-80	Sequence 80, Appl
36	840	41.3	351	12	US-10-145-128A-226	Sequence 226, App
37	840	41.3	351	12	US-10-184-642-80	Sequence 80, Appl
38	840	41.3	351	12	US-10-196-747-80	Sequence 80, Appl
39	840	41.3	351	12	US-10-173-689-80	Sequence 80, Appl
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41	840	41.3	351	12	US-10-173-691-80	Sequence 80, Appl
42	840	41.3	351	12	US-10-173-692-80	Sequence 80, Appl
43	840	41.3	351	12	US-10-173-694-80	Sequence 80, Appl
44	840	41.3	351	12	US-10-173-698-80	Sequence 80, Appl
45	840	41.3	351	12	US-10-173-699-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1

US-10-285-976-1

; Sequence 1, Application US/10285976

; Publication No. US20030165500A1

; GENERAL INFORMATION:

; APPLICANT: Rhee, Chae-Seo

```

; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leoni, Lorenzo M.
; APPLICANT: Corr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
; FILE REFERENCE: 023070-130320US
; CURRENT APPLICATION NUMBER: US/10/285,976
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wnt-1
US-10-285-976-1

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Query Match      100.0%; Score 2036; DB 12; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.3e-187;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGLWALLPGWVSATLLLLAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60
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Db      1 MGLWALLPGWVSATLLLLAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60

Qy     61 LQLLSRKQRRLLIRQNP GILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQLLSRKQRRLLIRQNP GILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120

Qy    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180
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Db    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180

Qy    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCTVRTCWMRLPTLR 240
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Db    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCTVRTCWMRLPTLR 240

Qy    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300
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Db    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300

Qy    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360
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Db    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360

Qy    361 THTRVLHECL 370
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Db    361 THTRVLHECL 370

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RESULT 2

US-10-028-248A-71

; Sequence 71, Application US/10028248A

; Publication No. US20030235882A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard

; APPLICANT: Patturajan, Meera

; APPLICANT: Vernet, Corine

; APPLICANT: Casman, Stacie

; APPLICANT: Malyankar, Uriel

; APPLICANT: Shenoy, Suresh

; APPLICANT: Spytek, Kimberly

; APPLICANT: Gangolli, Esha

; APPLICANT: Miller, Charles

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Smithson, Glennda

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Liu, Xiaohong

; APPLICANT: Colman, Steven

; APPLICANT: Tchernev, Velizar

; APPLICANT: Si, Jingsheng

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Sciore, Paul

; APPLICANT: Millet, Isabelle

; APPLICANT: Rothenberg, Mark

; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods of Use

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: 21402-222

; CURRENT APPLICATION NUMBER: US/10/028,248A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/256619

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/262959

; PRIOR FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 60/272408

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/285189

; PRIOR FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: 60/308039

; PRIOR FILING DATE: 2001-07-26

; PRIOR APPLICATION NUMBER: 60/311266

; PRIOR FILING DATE: 2001-08-09

; NUMBER OF SEQ ID NOS: 211

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 71

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: WNT domain

; OTHER INFORMATION: sequence

US-10-028-248A-71

Query Match 44.5%; Score 906; DB 12; Length 352;
Best Local Similarity 50.1%; Pred. No. 1.2e-78;
Matches 175; Conservative 51; Mismatches 83; Indels 40; Gaps 10;

Qy 60 SLQLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPH---LFGKI 116
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Db 4 SLPGLSPRQRLCRRNPDVMASVSEGAQLAIQECQHQFRGRRWNCSTLDSL NERSVFGKV 63

Qy 117 VNRCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRR-----RGPGGP 163
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Db 64 LKKGTRETAFFVYAISSAGVAHAVTRACSEGELESCGCDKRRKADEERLRIKLEPKGPGGP 123

Qy 164 --DWHWGGCSDNIDFGRLFGREFVDSGE-----KGRDLRFLMNLHNNEAGRTTVFSE 213
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Db 124 QGSWKWGGCSDNVEFGIRFSREFVDAREEREKLMTKSRDRDARSLMNLHNNEAGRKAVKSH 183

Qy 214 MRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRGSNR---ASRAE 270
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Db 184 MRRECKCHGVSGSCSLKTCWLSLPDFREVGDLLKEKYDGAIEVEVNRKGKQRSLSRKQ 243

Qy 271 LLRLEPEDPAHKPPSPH---DLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPAL---DG 324
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Db 244 ASALEAANERFKKPTRNQYTDLVYLEKSPDYCERDRETGSLGTQGRVCNKTSKGLQWRDG 303

Qy 325 CELLCCGRGHRTRTORV--TERCNCTFH--WCCHVSCRNCTHTRVLHEC 369
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Db 304 CELLCCGRGYNTE-QKVERTEKCNCKFHNGWCCYVKCEECTEVVEVHTC 351

RESULT 3

US-09-954-342-34

; Sequence 34, Application US/09954342
; Publication No. US20030170838A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, VISHNU S.
; APPLICANT: SPYTEK, KIMBERLY ANN
; APPLICANT: TAUPIER, RAYMOND J.
; APPLICANT: VERNET, CORINE A.
; APPLICANT: COLMAN, STEVEN D.
; APPLICANT: GORMAN, LINDA
; APPLICANT: TCHERNEV, VELIZAR T.
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: SHENOY, SURESH
; APPLICANT: PADIGARU, MURALIDHARA
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENNDA
; APPLICANT: MILLET, ISABELLE
; APPLICANT: PEYMAN, JOHN
; APPLICANT: STONE, DAVID
; APPLICANT: GUNTHER, ERIK
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: LI, LI
; APPLICANT: RASTELLI, LUCA
; APPLICANT: ZERHUSEN, BRYAN

Qy 195 RFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCVTRTCWMRLPTLRAVGDLRDRFDGAS 254
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 Db 180 RSAMNRHNNEAGRQAIASHMHLKCKCHGLSGSCEVKTCWWSQPDFRTIGDFLKDKYDSAS 239
 Qy 255 RVLYGNRGSNRASRAELLRLLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRA 314
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 Db 240 EMVV---EKHRESRGWVETLRPRYTYFKVPTERDLVYYEASPNFCEPNPETGSFGTRDRT 296
 Qy 315 CNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCTFWHCCHVSCRNCTHTRVLHEC 369
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 Db 297 CNVSSHGIDGCDLLCCGRGHNARTERRREKCHCVFWHCCYVSCQECTRVYDVHTC 351

RESULT 4

US-10-285-976-7

; Sequence 7, Application US/10285976
 ; Publication No. US20030165500A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rhee, Chae-Seo
 ; APPLICANT: Malini, Sen
 ; APPLICANT: Wu, Christina
 ; APPLICANT: Leoni, Lorenzo M.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
 ; TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
 ; FILE REFERENCE: 023070-130320US
 ; CURRENT APPLICATION NUMBER: US/10/285,976
 ; CURRENT FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: US 60/287,995
 ; PRIOR FILING DATE: 2001-05-01
 ; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
 ; PRIOR FILING DATE: 2002-05-01
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 355
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human Wnt-3
 US-10-285-976-7

Query Match 41.3%; Score 840.5; DB 12; Length 355;
 Best Local Similarity 46.0%; Pred. No. 2.4e-72;
 Matches 155; Conservative 52; Mismatches 121; Indels 9; Gaps 3;

Qy 34 WWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLRQNPGLHLSVSGGLQSAVREC 93
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 Db 26 WWSLALGQQYTSL-----GSQPLLCSIPGLVPKQLRFCRNYIEIMPSVAEGVKLG IQEC 80
 Qy 94 KWQFRNRRWNCPTAPGP-HLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCT 152
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 Db 81 QHQFRGRRWNCTTIDDSLAIFGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICG 140


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; PRIOR APPLICATION NUMBER: 60/238,398
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/232,675
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/274,862
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/233,801
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,676
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/233,960
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,402
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/233,521
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/233,522
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,679
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-342-36

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Query Match          41.3%; Score 840.5; DB 12; Length 355;
Best Local Similarity 46.0%; Pred. No. 2.4e-72;
Matches 155; Conservative 52; Mismatches 121; Indels 9; Gaps 3;

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Qy      34 WWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLIRQNPGLHLSVSGGLQSAVREC 93
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Db      26 WWSLALGQQYTSL-----GSQPLLCSIPGLVPKQLRFCRNYIEIMPSVAEGVKLGIQEC 80

Qy      94 KWQFRNRRWNCPTAPGP-HLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCT 152
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Db      81 QHQFRGRRWNCTTIDDSLAIFGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICG 140

Qy     153 CDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFS 212
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Db     141 CDSHHKGPPGEGWKWGGCSEDADFGVLVSREFADARENRPDARSAMNKHNNNEAGRTTILD 200

Qy     213 EMRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRGSNRRASRAELL 272
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Db     201 HMHLKCKCHGLSGSCEVKTCWWAQPDFRAIGDFLKDKYDSASEMVV---EKHRESRGWVE 257

Qy     273 RLEPEDPAHKPPSPHDLVYFEKSPNFCITYSGRLGTAGTAGRACNSSSPALDGCELLCCGR 332
      | :   |||: ||||:| |||| | :   |:| | || :| :|||:|||||
Db     258 TLRAKYSLFKPPTERDLVYYENSPNFCENPETGSFGTRDRTCNVTSHGIDGCDLLCCGR 317

Qy     333 GHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
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Db     318 GHNTRTEKRKEKCHCIFHWCCYVSCQECIRIYDVHTC 354

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RESULT 6

US-09-978-295A-226

; Sequence 226, Application US/09978295A

; Patent No. US20020156006A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C11

; CURRENT APPLICATION NUMBER: US/09/978,295A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR FILING DATE: 1998-05-07

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Best Local Similarity 44.8%; Pred. No. 2.7e-72;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

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Qy	74	QNPgilHsvSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIvNRGCREtAFiFAITSA	133
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Db	59	RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLpVFGKvVTQGTREAAfVYAISsa	118
Qy	134	GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDfGRlFGREFVDSGEKGR-	192
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Db	119	GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAfSQSFVDVRERSKG	178
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Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSpDFCEQDMRSGVLGT	291
Qy	311	AGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCnCTfHwCCHVScRNCTHTRVLHEC	369

DB

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RESULT 7

US-09-978-697-226

; Sequence 226, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C27

; CURRENT APPLICATION NUMBER: US/09/978,697

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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RESULT 8

US-09-978-192A-226

; Sequence 226, Application US/09978192A
 ; Patent No. US20020177553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
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Query Match          41.3%; Score 840; DB 10; Length 351;
Best Local Similarity 44.8%; Pred. No. 2.7e-72;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

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Qy      74 QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133
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Qy      134 GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGR- 192
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Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT	291
QY	311	AGRACNSSSPALDGCELLCCGRGHRTTRTQRVTERCNCCTFHWCCHVSCRNCTHTRVLHEC	369
Db	292	RGRTCNTSKAIDGCELLCCGRGFHTAQVELAERCSCKFWCCFVKCRQCQRLVELHTC	350

RESULT 9

US-09-999-832A-226

; Sequence 226, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Pacni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C63

; CURRENT APPLICATION NUMBER: US/09/999,832A

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29

Db	119	GVAFVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSNIAYGVAFSQSFDVRERSKG	178
Qy	193	--DLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLRDRF	250
Db	179	ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVPPFRQVGHALKEF	238
Qy	251	DGASRVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT	310
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT	291
Qy	311	AGRACNSSSPALDGCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRNCTHTRVLHEC	369
Db	292	RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTC	350

RESULT 10

US-09-978-189-226

; Sequence 226, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C7

; CURRENT APPLICATION NUMBER: US/09/978,189

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 41.3%; Score 840; DB 11; Length 351;
 Best Local Similarity 44.8%; Pred. No. 2.7e-72;
 Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY 14 TLLALAAALPAALANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLR 73
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 Db 9 SLRLLVFAVFSAAASN-----WLYLAKLSSVGSISEETCE-----KLKGLIQRQVQMCK 58
 QY 74 QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133

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      :| :| || | | |: ||:||||||| | :|||:| :| || ||:|:|
Db      59 RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFYAIISSA 118
QY      134 GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGR- 192
      || :| |:|| | :| | || | :| | ||||| :| | : ||| |: :
Db      119 GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFDVDRERSKG 178
QY      193 --DLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGSCTVRTCWMRLPTLRAVGDVLRDRF 250
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Db      179 ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVPPFRQVGHALKEKF 238
QY      251 DGASRVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310
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Db      239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT 291
QY      311 AGRACNSSSPALDGCELLCCGRGHRTTRTQVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
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RESULT 11

US-09-978-608A-226

; Sequence 226, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C22

; CURRENT APPLICATION NUMBER: US/09/978,608A

; CURRENT FILING DATE: 2001-10-16

; Publication No. US20030050239A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C4

; CURRENT APPLICATION NUMBER: US/09/978,191A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
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; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR APPLICATION NUMBER: 60/081952
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; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598

Query Match 41.3%; Score 840; DB 11; Length 351;
Best Local Similarity 44.8%; Pred. No. 2.7e-72;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY	14	TLLLALAAALPAALAAANSSGRWWGIVNVASSTNLLTDSLSQLVLEPSLQLLLSRKQRRILIR	73
Db	9	SLRLLLVFAVFSAAASN-----WLYLAKLSSVGSISEEETCE-----KLKGLIQRQVQMCK	58
QY	74	QNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS	133
Db	59	RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVTQGTREAAFYAIISS	118
QY	134	GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRFLGREFVDSGEKGR	192
Db	119	GVAVAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFDVDRERSKG	178
QY	193	--DLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLVRDRF	250
Db	179	ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCVKTWRAVPPFRQVGHALKEKF	238
QY	251	DGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT	310
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT	291
QY	311	AGRACNSSSPALDGCELLCCGRGHRTRTQVTERCNCTFWCCCHVSCRNCTHTRVLHEC	369
Db	292	RGRTCNTKSKAIDGCELLCCGRGFHTAQVELAERCSCFKFWCCFVKRCQRCQLVLELHTC	350

RESULT 14

US-09-978-403A-226

; Sequence 226, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

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; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

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; PRIOR FILING DATE: 1998-03-11

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; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 41.3%; Score 840; DB 11; Length 351;
Best Local Similarity 44.8%; Pred. No. 2.7e-72;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

Qy	14	TLALLAALPAALAANSSGKWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLR	73
Db	9	SLRLLVFAVFSAAASN-----WLYLAKLSSVGSISEEETCE-----KLKGLIQRQVQMCK	58
Qy	74	QNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS	133
Db	59	RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVTQGTREAAFVYAISS	118
Qy	134	GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGCSNIDFGRLFGREFVDSGEKGR-	192
Db	119	GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSNIAYGVAFSQSFDVDRERSKG	178
Qy	193	--DLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLRDRF	250
Db	179	ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVPPFRQVGHALKEKF	238
Qy	251	DGASRVLYGNRGSNRASRAELRLLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT	310
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEODMRSGVLGT	291

QY 311 AGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCCTFHWCCHVSCRNCTHTRVLHEC 369
|| || :| |:||||||| | : |||:| ||||| | || | || |
Db 292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCCKFHWCCFVKCRQCQRLVELHTC 350

RESULT 15

US-09-978-564A-226

; Sequence 226, Application US/09978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin R.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C25

; CURRENT APPLICATION NUMBER: US/09/978,564A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

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; PRIOR FILING DATE: 1998-05-05
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441

Qy	251	DGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT	310
		: : : : :	
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT	291
Qy	311	AGRACNSSSPALDGCELLCCGRGHRTTRTQVTERCNCTFHWCCHVSCRNCTHTRVLHEC	369
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Db	292	RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCCKFWCCFVKCRQCQRLVELHTC	350

Search completed: January 21, 2004, 10:53:22
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 21, 2004, 10:46:52 ; Search time 22 Seconds
(without alignments)
711.592 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2036
Sequence: 1 MGLWALLPGWVSATLLLLALA.....WCCHVSCRNCTHTRVLHECL 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	2036	100.0	370	4	US-09-417-039-3
2	840.5	41.3	355	3	US-09-082-270-2
3	834	41.0	351	3	US-09-067-782A-2
4	785	38.6	360	4	US-09-417-039-4
5	756.5	37.6	365	4	US-09-417-039-9
6	756	37.1	397	1	US-08-647-928-8
7	731.5	35.9	372	3	US-09-082-089-2
8	723.5	35.5	359	3	US-09-082-089-3
9	723.5	35.5	363	3	US-09-082-089-5
10	720.5	35.4	349	3	US-09-459-774-2
11	720.5	35.4	349	4	US-09-903-817-2

12	713.5	35.0	349	4	US-09-417-039-7	Sequence 7, Appli
13	709.5	34.8	389	2	US-08-485-449-2	Sequence 2, Appli
14	709.5	34.8	389	2	US-08-485-449-7	Sequence 7, Appli
15	707	34.7	389	2	US-08-485-449-6	Sequence 6, Appli
16	679	33.3	376	2	US-08-485-449-5	Sequence 5, Appli
17	401.5	19.7	133	4	US-09-417-039-5	Sequence 5, Appli
18	373.5	18.3	159	3	US-09-082-270-4	Sequence 4, Appli
19	336.5	16.5	121	3	US-09-067-782A-5	Sequence 5, Appli
20	327.5	16.1	120	4	US-09-417-039-6	Sequence 6, Appli
21	284.5	14.0	124	4	US-09-417-039-8	Sequence 8, Appli
22	225	11.1	131	3	US-09-067-782A-4	Sequence 4, Appli
23	113.5	5.6	115	2	US-08-485-449-4	Sequence 4, Appli
24	113	5.6	577	4	US-09-252-991A-25632	Sequence 25632, A
25	99.5	4.9	329	4	US-09-252-991A-30436	Sequence 30436, A
26	99	4.9	956	1	US-08-185-232A-2	Sequence 2, Appli
27	99	4.9	956	1	US-08-416-523-2	Sequence 2, Appli
28	99	4.9	956	3	US-08-789-478-2	Sequence 2, Appli
29	96	4.7	399	4	US-09-553-498-2	Sequence 2, Appli
30	96	4.7	399	4	US-09-618-869-2	Sequence 2, Appli
31	92	4.5	477	4	US-09-252-991A-24574	Sequence 24574, A
32	91	4.5	519	3	US-09-211-704A-7	Sequence 7, Appli
33	89.5	4.4	1652	4	US-09-627-650B-1	Sequence 1, Appli
34	89.5	4.4	1652	4	US-09-436-063C-1	Sequence 1, Appli
35	89.5	4.4	1917	4	US-09-627-650B-5	Sequence 5, Appli
36	89.5	4.4	1917	4	US-09-436-063C-5	Sequence 5, Appli
37	89.5	4.4	2508	4	US-09-627-650B-7	Sequence 7, Appli
38	89.5	4.4	2508	4	US-09-436-063C-7	Sequence 7, Appli
39	89.5	4.4	2544	4	US-09-627-650B-3	Sequence 3, Appli
40	89.5	4.4	2544	4	US-09-436-063C-3	Sequence 3, Appli
41	89.5	4.4	2601	4	US-09-627-650B-9	Sequence 9, Appli
42	89.5	4.4	2601	4	US-09-436-063C-9	Sequence 9, Appli
43	89	4.4	605	1	US-08-152-019A-26	Sequence 26, Appli
44	89	4.4	605	3	US-08-482-677-4	Sequence 4, Appli
45	89	4.4	605	3	US-08-650-599A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-417-039-3

; Sequence 3, Application US/09417039A

; Patent No. 6485972

; GENERAL INFORMATION:

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Parr, Brian A.

; APPLICANT: Vaino, Seppo

; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS

; FILE REFERENCE: 00246/232001

; CURRENT APPLICATION NUMBER: US/09/417,039A

; CURRENT FILING DATE: 1999-10-12

; EARLIER APPLICATION NUMBER: US 60/109,355

; EARLIER FILING DATE: 1998-10-15

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 370

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-039-3

Query Match 100.0%; Score 2036; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-199;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60

Qy     61 LQLLSRKQRRLLRQNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQLLSRKQRRLLRQNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120

Qy    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180

Qy    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240

Qy    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300

Qy    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRNC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRNC 360

Qy    361 THTRVLHECL 370
        ||||||||
Db    361 THTRVLHECL 370
```

RESULT 2

US-09-082-270-2

; Sequence 2, Application US/09082270

; Patent No. 6043053

; GENERAL INFORMATION:

; APPLICANT: BARNES, MICHAEL

; APPLICANT: TESTA, TANIA

; TITLE OF INVENTION: No. 6043053e1 Compounds

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

```

; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,270
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9710716.3
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: GB 9804921.6
; FILING DATE: 06-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30164
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-082-270-2

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Query Match          41.3%; Score 840.5; DB 3; Length 355;
Best Local Similarity 46.0%; Pred. No. 1.8e-77;
Matches 155; Conservative 52; Mismatches 121; Indels 9; Gaps 3;

```

```

Qy      34 WWGIVNVASSTNLLTDSKSIQLVLEPSLQLLSRKQRRLIRQNPGILHSVSGGLQSAVREC 93
      || :   :|:|   | :| | :| | | | | :| :| :| :| :| :|
Db      26 WWSLALGQQYTSL-----GSQPLLCSIPGLVPKQLRFCRNYIEIMPSVAEGVKLGIQEC 80

Qy      94 KWQFRNRRWNCPTAPGP-HLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCT 152
      : ||| ||||| |   :|| :::: ||:|: || |||| :| |||:|: |
Db      81 QHQFRGRRWNCTTIDDSLAIFGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICG 140

Qy     153 CDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRITTVFS 212
      || :|| | | |||||:: ||| | ||| |: | | | ||||| |||:
Db     141 CDSHHKGPPGEGWKWGGCSEDADFGVLVSREFADARENRPDARSAMNKHNEAGRITILD 200

Qy     212 EMRQECKCHGMSGSCTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRGSNRASRAELL 272
      | :||| |:||| | :|| | | ||:| |:|:| || ::   :| || :
Db     201 HMHLKCKCHGLSGSCEVKTCWQAQPDFRAIGDFLKDKYDSASEMVV---EKHRESRGWVE 257

Qy     273 RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGR LGTAGTAGRACNSSSPALDGCELLCCGR 332
      | :   |||: ||||:| ||||| :   |: || | || :| :|||:| ||||
Db     258 TLRAKYSLFKPPTERDLVYYENSPNFCEPNPETGSFGTRDRCNVTSHGIDGCDLLCCGR 317

Qy     333 GHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
      || |||:| :|:| ||||:| ||| :| |
Db     318 GHNTRTEKRKEKCHCIFHWCCYVSCQECIRIYDVHTC 354

```


Qy	134	GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRFLFGREFVDSGEKGR-	192
		: : : : : : : :	
Db	119	GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFGQWSGCSDNIAYGVAFSQSFSVDVRERSKG	178
Qy	193	--DLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGCTVVRTCWMRLPTLRAVGDLRDRF	250
		: : : : : : :	
Db	179	ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKT CWRAVPPFRQVGHALKEKF	238
Qy	251	DGASRVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTYSGR LGTAGT	310
		: : : : :	
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT	291
Qy	311	AGRACNSSSPALDGCCELLCCGRGHRTTRTQRVTERCNCFTFWCCHVSCRNCTHTRVLHEC	369
		: : : :	
Db	292	RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTC	350

UJS-09-417-039-4

Patent No. 6485972

APPLICANT: McMahon, Andrew P.

7. APPLICANT: Vaino, Seppo

FILE REFERENCE: 00246/232001

CURRENT FILING DATE: 1999-10-12

EARLIER FILING DATE: 1998-10-15

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 360

; ORGANISM: Homo sapiens

Query Match 38.6%; Score 785; DB 4; Length 360;

Matches 150; Conservative 63; Mismatches 124; Indels 36; Gaps 7;

Q_Y 2 GLWALLPGWVSATLLLALAALPAALAANSSGRWWGI'NVASSTNLLTDSKSLQLVLEPSL 61

7. GIWLWLP-----LLLTW-----LTPEVNSSWWYMRATGGSSRVMCD-----NV 44

Qy 62 QLLSRKQRRLLIRQNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPH-LFGKIVNRG 120.

Db 45 PGLVSSOROLCHRHPDVMRAISOGVAEWTAECOHOFRHRWNCNTLDRDHS LFGRVLLRS 104

Qv 121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPD---WHWGGCSDNIDFG 177

Db 105 SRESAFVYA ISSAGVVFAITRAC SOGEVKSCSCDPKKMGS AKDSKGI FDWGGCSDNIDYG 164

178 RLFGREFVDSGE-KGRDLRFLMNLHNNEAGRRTTVFSEMROECKCHGMSGSCTVRTCWMRL 236

Query Match 37.1%; Score 756; DB 1; Length 397;
 Best Local Similarity 41.0%; Pred. No. 8.6e-69;
 Matches 152; Conservative 62; Mismatches 119; Indels 38; Gaps 9;

```

QY      11 VSATLLLLAALPAALANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRR 70
      :: ||| | ||| : : || | : : | : :: | : ||:
Db      41 LACLLLLLLLLTLPARVDTS----WWYIGALGAR-----VICDNIPGLVSRQRQ 84

QY      71 LIRQNPgilHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPH-LFGKIVNRGCRETAFIFA 129
      | :: | | : || | : : ||| : ||| : ||| | | : ||| :: | | : |||
Db      85 LCQRYPDIMRSVGEGAREWIRECQHQRHHRWNCTTLDRDHTVFGRVMLRSSRDGAFVYA 144

QY     130 ITSAGVTHSVARSCSEGSIESCTCDYRRRG---PGGPDWHWGGCSDNIDFGRLFGREFVD 186
      | : ||| | :: | : ||| : | : | : || | | : | ||||| | : | | : |||
Db     145 ISSAGVVHAITRACSQGELSVCSDPYTRGRHHDQRGDFDWGGCSDNIHYGVRFAKAFVD 204

QY     187 SGEKG-RDLRFLMNLHNEAGRT-----TVFSEMRQECKCHGMSGCTVRTCWMRLPTL 239
      : || : | | ||||| ||| | : : ||||| : ||||| : ||| |
Db     205 AKEKRLKDARALMNLHNNRCGRTVSTHVCARRRFLKLECKCHGVSGSCTLRTCWRLSDF 264

QY     240 RAVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFC 299
      | || || | ||| :| : | : : : : : ||| : ::|
Db     265 RRTGDYLRRTDGAQVQMATQDGANFTAARQ-----GYRRATRTDLVYLTTPADYC 315

QY     300 TYSGRGLGTAGTAGRACNSSSPALDGCCELLCCGRGH-RTRTQRVTERCNCTFHWCCHVSCR 358
      | : |||| | : : | |||| : |||| : || | |||| | | :
Db     316 VLDKAAGSLGTAGRVCSKTSKGTDGCEIMCCGRGYDTTRVTRVTQ-CECKFHWCCAVRCK 374

QY     359 NCTHTRVLHEC 369
      | : | : |
Db     375 ECRNTVDVHTC 385
  
```

RESULT 7

US-09-082-089-2

; Sequence 2, Application US/09082089

; Patent No. 6100060

; GENERAL INFORMATION:

; APPLICANT: BARNES, MICHAEL

; APPLICANT: TESTA, TANIA

; APPLICANT: KELSELL, DAVID

; TITLE OF INVENTION: No. 6100060el Compounds

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,089
 FILING DATE: 20-MAY-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9710737.9
 FILING DATE: 23-MAY-1997
 APPLICATION NUMBER: GB 9803981.1
 FILING DATE: 25-FEB-1998
 APPLICATION NUMBER: GB 9804007.4
 FILING DATE: 25-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-30166
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-082-089-2

Query Match 35.9%; Score 731.5; DB 3; Length 372;
 Best Local Similarity 38.5%; Pred. No. 2.5e-66;
 Matches 145; Conservative 67; Mismatches 130; Indels 35; Gaps 7

QY 2 GLWALLPGWVSATLILALALPAALA-----ANSSGRWWGIVNVASSTNLLTDSKSLQLV 56
 | | | : : | | | : | | | : : : : :
 Db 5 GHWGGLRPTMPSLLLLFTAALLSSWAQLLTDANS---WWSL-----ALNPVQRPEMFIIG 56
 QY 57 LEP---SLQLLSRKQRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLF 113
 : | | | | : : : : : : : : : : : : : :
 Db 57 AQPVCSQLPGLSPGQRKLCQLYQEHMAYIREGAKTGIKECQHQPQRRWKSTADNASVF 116
 QY 114 GKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGP-DWHWGGCSD 172
 | : : | | | | | : : : | : | : : | : | : | : | : | : | : | :
 Db 117 GRVMQIGSRETAFTHAVSAAGVVNAISPACSEGELSTCGCSRTARPKDLPRDWLWGGCGD 176
 QY 173 NIDFGRLFGREFVDSGEKGRDL-----RFLMNLHNNEAGRTTVFSEMRQECKCHGMS 224
 | : : | | : | | : : : : | | | | | | | : : | | | : | : | :
 Db 177 NVEYGYRFAKEFVDAREEREKNFAKGSEEQGRVLMNLQNEAGRRAVYKMADVACKCHGVS 236
 QY 225 GSCTVRTCWMRLPTLRAVGDLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPP 284
 | | : : | | : : | | | : : : | : : : : | | : : | :
 Db 237 RSCRLKTCWLQLAEFRKVGDRLEKEKYDSAAAMRVTRKG-----RLELVNSRFTQP 286
 QY 285 SPHDLVYFEKSPNFCTYSGRLGTAGTAGACNSSSPALDGCELLCCGRGHRTRTQRVTER 344
 : | | | : : : : : : : | : | | | : : : : : : : : : :
 Db 287 TPEDLVYVDPSPDYCLRNESTGSLGTQGRLCNKTSEGMDGCELMCCGRGYNQFKSVQVER 346
 QY 345 CNCTFHWCCHVSCRNCT 361
 : | | | | | : : |

Db

347 CHCKFWCCFVRCKKCT 363

RESULT 8

US-09-082-089-3

; Sequence 3, Application US/09082089

; Patent No. 6100060

; GENERAL INFORMATION:

; APPLICANT: BARNES, MICHAEL

; APPLICANT: TESTA, TANIA

; APPLICANT: KELSELL, DAVID

; TITLE OF INVENTION: No. 6100060el Compounds

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082,089

; FILING DATE: 20-MAY-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9710737.9

; FILING DATE: 23-MAY-1997

; APPLICATION NUMBER: GB 9803981.1

; FILING DATE: 25-FEB-1998

; APPLICATION NUMBER: GB 9804007.4

; FILING DATE: 25-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F.

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-30166

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-082-089-3

Query Match 35.5%; Score 723.5; DB 3; Length 359;

Best Local Similarity 39.0%; Pred. No. 1.6e-65;

Matches 142; Conservative 65; Mismatches 122; Indels 35; Gaps 7;

Qy 15 LLLALAALPAALA-----ANSSGRWWGIVNVASSTNLLTDSKSLQLVLEP---SLQLLSR 66
 ||| ||| :: | ||| || : : : : : ||
 Db 5 LLLFTAALLSSWAQLLTDANS---WWSL-----ALNPVQRPEMFIIGAQPVCSQLPGLSP 56

Qy 67 KQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAF 126
 ||:| : : : | :: ::||: || ||| | || :||::: | |||||
 Db 57 GQRKLCQLYQEHMAYIREGAKTGIKECQHQPQRRWKCSTADNASVFGRVMQIGSRETAF 116

Qy 127 IFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGP-DWHWGGCSDNIDFGRLFGREFV 185
 |::||| ::::|:|||| : :| | | | ||| ||:::| | :|||
 Db 117 THAVSAAGVVNAISRACSEGELSTCGCSRTARPKDLPRDWLWGGCGDNVEYGYRFAKEFV 176

Qy 186 DSGEKGRDL-----RFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGSCVTRTCWMRLP 237
 |: |: :: | |||| ||||| |: |||||:| || ::|||::|
 Db 177 DAREREKNFAKGSEEQGRVLMNLQNEAGRRVYKMADVACKCHGVSRSCRLKTCWLQLA 236

Qy 238 TLRAVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPN 297
 | ||| |:::| |: : :| ||| : |:| |||| : ||:
 Db 237 EFRKVGDRLEKEYDSAAAMRVTRKG-----RLELVNSRFTQPTPEDLVYVDPSPD 286

Qy 298 FCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCNTHWCCHVSC 357
 :| : |: || || || :| :|||:| ||||: |||:| ||||| | |
 Db 287 YCLRNESTGSLGTQGRLCNKTSEGMDGCELMCCGRGYNQFKSVQVERCHCKFHWCCFVRC 346

Qy 358 RNCT 361
 : ||
 Db 347 KKCT 350

RESULT 9

US-09-082-089-5

; Sequence 5, Application US/09082089

; Patent No. 6100060

; GENERAL INFORMATION:

; APPLICANT: BARNES, MICHAEL

; APPLICANT: TESTA, TANIA

; APPLICANT: KELSELL, DAVID

; TITLE OF INVENTION: No. 6100060e1 Compounds

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082,089

; FILING DATE: 20-MAY-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9710737.9

FILING DATE: 23-MAY-1997
 APPLICATION NUMBER: GB 9803981.1
 FILING DATE: 25-FEB-1998
 APPLICATION NUMBER: GB 9804007.4
 FILING DATE: 25-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-30166
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 363 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-082-089-5

Query Match 35.5%; Score 723.5; DB 3; Length 363;
 Best Local Similarity 39.0%; Pred. No. 1.6e-65;
 Matches 142; Conservative 65; Mismatches 122; Indels 35; Gaps 7;

Qy	15	LLJALAAALPAALA-----ANSSGRWWGIVNVASSTNLLTDSKSLQLVLEP---SLQLLSR	66
Db	9	LLLFTAALLSSWAQLLTDANS---WWSL-----ALNFVQRPEMFLIGAQPVCSQLPGLSP	60
Qy	67	KQRRLIRQNPGILHSVSGGLOSARECKWQFNRNRWNCPTAPGPHLFGKIVNRGCRETAF	126
Db	61	GQRKLCQLYQEHMAYIREGAKTGIKECQHQPORRWKCSTADNASVFGRVMQIGSRETAF	120
Qy	127	IFAITSAAGVTHSVARSCSEGSIESCTCDYRRRGPGGP-DWHWGGCSDNIDFGRLFGREFV	185
Db	121	THAVSAAGVVNAISRACSEGELSTCGCSRTARPKDLPRDWLWGGCGDNVEYGYRFAKEFV	180
Qy	186	DSGEKGRDL-----RFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLP	237
Db	181	DAREREKNFAKGSEEQGRVLMNLQNEAGRRVYKMAADVACKCHGVSRSCRLKTCWLQLA	240
Qy	238	TLRAVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKKPPSPHDLVYFEKSPN	297
Db	241	EFRKVGDRLEKEKYSAAAMRVTRKG-----RLELVNSRFTQPTPEDLVYVDPSPD	290
Qy	298	FCTYSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSC	357
Db	291	YCLRNESTGSLGTQGRLCNKTSEGMDGCELMCCGRGYNQFKSVQVERCHCKFHWCCFVRC	350
Qy	358	RNCT	361
Db	351	KKCT	354

```
; Sequence 2; Application US/09459774
; Patent No. 6297030
; GENERAL INFORMATION:
; APPLICANT: Michael Robert Barnes
; APPLICANT: Tania Tamson Testa
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30193
; CURRENT APPLICATION NUMBER: US/09/459,774
; CURRENT FILING DATE: 1999-12-13
; EARLIER APPLICATION NUMBER: UK 9828419.3
; EARLIER FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-459-774-2
```

```
Query Match          35.4%; Score 720.5; DB 3; Length 349;
Best Local Similarity 42.2%; Pred. No. 3e-65;
Matches 130; Conservative 57; Mismatches 116; Indels 5; Gaps 3;
```

```
QY      64 LSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRE 123
      | : || : : | : : | | : || : || | || | : || | : | ||
Db      44 LAPRQRAICQSRPDALIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSR 103

QY      124 TAFIEAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPD--WHWGGCSDNIDFGRLFG 181
      || : || : || | : : : : : | || : | | || | : : | |
Db      104 AAFTYAIIAAGVAHAITAACQGNLSDCGCDKEKQGQYHRDEGWKGCCSADIRYGIGFA 163

QY      182 REFVDSGEKGRDLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGCTVTCWMKRLPTLRA 241
      : || | : | : : | || || || || | : : | || || : || | || |
Db      164 KVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPPQFRE 223

QY      242 VGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTY 301
      : | || : : : | | | : | | : : : : : | || | || || : |
Db      224 LGYVLKDKYNEAVHVEPVVRASRNK--RPTFLKIK-KPLSYRKPMDTDLVYIEKSPNYCEE 280

QY      302 SGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNCT 361
      | : || || || | : | | : : || | : | : || || || | : | :
Db      281 DPTGSGVTQGRACNKTAPQASGCDLMCCGRGYNTHQYARVWQCNCCKFHWCCYVKCNTCS 340

QY      362 HTRVLHEC 369
      : : |
Db      341 ERTEMYTC 348
```

RESULT 11

US-09-903-817-2

```
; Sequence 2; Application US/09903817
; Patent No. 6515108
; GENERAL INFORMATION:
; APPLICANT: BARNES, Michael Robert
; APPLICANT: TESTA, Tania Tamson
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30193-D1
```

; CURRENT APPLICATION NUMBER: US/09/903,817
 ; CURRENT FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: UK 9828419.3
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 09/459,774
 ; PRIOR FILING DATE: 1999-12-13
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 349
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-903-817-2

Query Match 35.4%; Score 720.5; DB 4; Length 349;
 Best Local Similarity 42.2%; Pred. No. 3e-65;
 Matches 130; Conservative 57; Mismatches 116; Indels 5; Gaps 3;

Qy 64 LSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRE 123
 |: :|| : : | : : | | : ||::||| ||| :||| : | ||
 Db 44 LAPRQRAICQSRPDAAIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSR 103
 Qy 124 TAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPD--WHWGGCSDNIDFGRLFG 181
 || :|| :||| |:: :||::| : || :| | |||| :| :| |
 Db 104 AAFYAIIAAGVAHAITAACQGNLSDCGCDKEKQGQYHRDEGWKGWGCADIRYGIGFA 163
 Qy 182 REFVDSGEKGRDLRFLMNLHNNEAGRITVFSEMRQECKCHGMSGCTVRTCWMRLPTLRA 241
 : ||| : | : : | ||||| ||| : : | ||||| : ||| | | |
 Db 164 KVPYDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPQFRE 223
 Qy 242 VGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCTY 301
 : | ||| : || : | : | : : : : : | ||| ||||| : |
 Db 224 LGYVLKDKYNEAVHVEPVVRASRNK--RPTFLKIK-KPLSYRKPMDTDLVYIEKSPNYCEE 280
 Qy 302 SGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRNCT 361
 | : || ||||| :| ||| : ||||| : | : ||| ||||| : | | :
 Db 281 DPVTGSGVTQGRACNKTAPQASGCDLMCCGRGYNTHQYARVWQCNCCKFHWCCYVKCNTCS 340
 Qy 362 HTRVLHEC 369
 : : |
 Db 341 ERTEMYTC 348

RESULT 12

US-09-417-039-7

; Sequence 7, Application US/09417039A
 ; Patent No. 6485972
 ; GENERAL INFORMATION:
 ; APPLICANT: McMahon, Andrew P.
 ; APPLICANT: Parr, Brian A.
 ; APPLICANT: Vaino, Seppo
 ; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS
 ; FILE REFERENCE: 00246/232001
 ; CURRENT APPLICATION NUMBER: US/09/417,039A
 ; CURRENT FILING DATE: 1999-10-12
 ; EARLIER APPLICATION NUMBER: US 60/109,355
 ; EARLIER FILING DATE: 1998-10-15


```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/485,449
;   FILING DATE:
;   CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  KONSKI, ANTOINETTE F.
;   REGISTRATION NUMBER:  34,202
;   REFERENCE/DOCKET NUMBER:  20296-20035.00
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 813-5600
;   TELEFAX:  (415) 494-0792
;   TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  389 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-98-485-449-2

```

```

Query Match      34.8%;  Score 709.5;  DB 2;  Length 389;
Best Local Similarity  38.5%;  Pred. No. 4.6e-64;
Matches  153;  Conservative  53;  Mismatches 122;  Indels  69;  Gaps  10;

```

```

QY      32 PAALAANSSGRWWGIVNVASSTNLLTDS-KSLQLVLEP-----SLQLLSRKQRRLI 72
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      11 PSGLA-----GLLFLALCSRALSNELGLKLPGEFPLTGNTVCLTSLGSLSKRQLGLC 62

QY      73 RQNPGLIHSVSGGLQSAVRECKWQFRNRWNCPTAPG----PHLFGKIVNRGCRETAFIF 128
      :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      63 LPNEDVTASALQGLHIAVHECQHLRQDRWNCSALEGGGRLPH-HSAILKRGFRESAFSE 121

QY     129 AITSAGVTHSVARSCSEGSIESCTCDYRRRG----- 159
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     122 SMLAAGVMHAVATACSLGKLVSCCGGWKGSGEQDRLRAKLLQLQALS RGKSFPHSLPSPG 181

QY     160 -----PGGPD-WHWGGCSDNIDFGRLEFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFS 212
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     182 PGSSPSPGPQDTWEWGGCNHMDDFGEKFSRDFLDSREAPRDIQARMRIHNNRVGRQVVTE 241

QY     213 EMRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRGSNRASRAELL 272
      ::::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     242 NLKRKCKCHGTSGSCQFKTCWRAAPEFRAVGAALRERL---GRAIFIDT-HNRNSGAFQP 297

QY     273 RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGR 332
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     298 RLRPRRLS-----GELVYFEKSPDFCERDPTMGSPGTRGRACNKTSRLLDGCGSLCCGR 351

QY     333 GHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     352 GHNVLRLQTRVERCHCRFHWCCYVLCDECKVTEWVNVC 388

```

; Sequence 7, Application US/08485449
; Patent No. 5824789
; GENERAL INFORMATION:
; APPLICANT: VANDENBERG, DAVID
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,449
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20296-20035.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-449-7.

Query Match 34.8%; Score 709.5; DB 2; Length 389;
Best Local Similarity 38.5%; Pred. No. 4.6e-64;
Matches 153; Conservative 53; Mismatches 122; Indels 69; Gaps 10;

Qy 23 PAALANSSGRWWGIVNVASSTNLLTDS-KSLQLVLEP-----SLQLLSRKQRRLI 72
|: || |:::| : |:: |:: | |::| |
Db 11 PSGLA-----GLLFLALCSRALSNELGLKLPGEPLTGNTVCLTSLGSLSKRQLGLC 62
QY 73 RQNPgilHsvSgGLQSAVRECKWQFRNRWNCPTAPG----PHLFGKIVNRGCRETAFIF 128
: || : | || || ||: | |::||| | || |: || ||: || |
Db 63 LRNPdVTASALQGLHIAVHECQHQLRDQRWNCSALEGGGRLPH-HSAILKRGFRESAFSF 121
Qy 129 AITSAGVTHSvarScSEGSIESCTCDYRRRG----- 159
:: : ||| |::| |:: | |:: | |:: |
Db 122 SMLAAGVMHAVATACSLGKLVSCGCGWKSGEQDRLRAKLLQLQALSrgKsfPhSLPSPG 181
Qy 160 -----PGGPD-WHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFS 212

Db 182 PGSSPSPGPQDTWEWGGCNHDMDFGEKFSRDFLDSREAPRDIQARMRIHNNRVGRQVVTE 241
 Qy 213 EMRQECKCHGMSGSCVTRTCWMRLPTLRAVGDLRDRFDGASRVLYGNRGSNRASRAELL 272
 Db 242 NLKRKCKCHGTSGSCQFKTCWRAAPEFRAVGAALRERL---GRAIFIDT-HNRNSGAFQP 297
 Qy 273 RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGR LGTAGTAGRACNSSSPALDGCELLCCGR 332
 Db 298 RLRPRRLS-----GELVYFEKSPDFCERDPTMGSPGTRGRACNKTSRLLDGCGSLCCGR 351
 Qy 333 GHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
 Db 352 GHNVLQRQTRVERCHCRFWCCYVLCDECKVTEWVNV 388

RESULT 15

US-08-485-449-6

; Sequence 6, Application US/08485449

; Patent No. 5824789

; GENERAL INFORMATION:

; APPLICANT: VANDENBERG, DAVID

; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

; TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,449

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: KONSKI, ANTOINETTE F.

; REGISTRATION NUMBER: 34,202

; REFERENCE/DOCKET NUMBER: 20296-20035.00

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 389 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-485-449-6

Query Match 34.7%; Score 707; DB 2; Length 389;
 Best Local Similarity 39.6%; Pred. No. 8.4e-64;
 Matches 149; Conservative 48; Mismatches 119; Indels 60; Gaps 8;

```

Qy      43 STNLLTDSKSLQLVLEP-----SLQLLSRKQRRLLRQNPGILHSVSGGLQSAVREC 93
      | | : | : | | : | | : | | : | | | | |
Db      24 SRALSNEILGLKLPGEPLTANTVCLTSLGLSKRQLGLCLRSPDVTASALQGLHIAVHEC 83

Qy      94 KWQFRNRRWNCPTAPG----PHLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIE 149
      : | : : | | | | | | | | : | | | | : | | : | | | :
Db      84 QHQLRDQRWNCSALEGGGRLPH-HSAILKRGFRESAFSFSMLAAGVMHAVATACSLGKLV 142

Qy     150 SCTCDYRRRG-----PGGPD-WHWGGCSDN 173
      | | | : | | | | | | | | | | | | : :
Db     143 SCGCGWKGSGEQDRLRAKLLQLQALSRGKIFPISQSPVPGSVPSGPQDTWEWGGCNHD 202

Qy     174 IDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRITTFSEMRQECKCHGMSGCTVRTCW 233
      : | | | | | : | : | | | | | : | | | | | : | | | : | |
Db     203 MDFGEKFSRDFLDSREAPRDIQARMRIHNNRVGRQVV TENLKRKCKCHGTSGSCQPKTCW 262

Qy     234 MRLPTLRAVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFE 293
      | | | : | | : | | : : | | | | | | : : | | | |
Db     263 RAAPEFRAIGAALRERJ---SRAIFIDT-HNRNSGAFQPRLRPRRLS-----GELVYFE 312

Qy     294 KSPNFCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFWCC 353
      | | | : | | : | | | | | | | | | | | | | | | | | |
Db     313 KSPDFCERDFTLGSPGTRGRACNKTSRLLDGCGSLCCGRGHNVLRQTRVERCHCRFWCC 372

Qy     354 HVSCRNCTHTRVIHEC 369
      : | | | | | : | |
Db     373 YVLCDECKVTEWVNVC 388
  
```

Search completed: January 21, 2004, 10:52:31
 Job time : 23 secs

OM protein - protein search, using sw model

Run on: January 21, 2004, 10:43:57 ; Search time 42 Seconds
(without alignments)
2273.321 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2036
Sequence: 1 MGLWALLPGWVSATLLLLALA.....WCCHVSCRNCTHTRVLHECL 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description

1	1598	78.5	370	13	P79752	P79752 fugu rubrip
2	1203.5	59.1	262	13	Q9PT79	Q9pt79 oryzias lat
3	1151	56.5	394	5	Q9GRA6	Q9gra6 gryllus bim
4	1127.5	55.4	374	5	Q8T396	Q8t396 cupiennius
5	1064.5	52.3	377	5	O61699	O61699 branchiosto
6	1037	50.9	358	5	Q8MPL8	Q8mpl8 platynereis
7	1018.5	50.0	468	5	Q8MQP9	Q8mqp9 drosophila
8	996.5	48.9	337	5	Q8MZJ5	Q8mzj5 pheidole mo
9	990.5	48.6	415	5	Q8IPI1	Q8ipi1 drosophila
10	989	48.6	334	5	Q8MZJ2	Q8mzj2 formica nit
11	971	47.7	337	5	Q8MZJ4	Q8mzj4 crematogast
12	950.5	46.7	330	5	Q8MZJ3	Q8mzj3 myrmica ame
13	878.5	43.1	365	5	Q8WRF7	Q8wrf7 mysidium co
14	866.5	42.6	303	5	Q9TX64	Q9tx64 tribolium c
15	838	41.2	351	4	Q8IUM6	Q8ium6 homo sapien
16	834	41.0	353	5	Q9TZT6	Q9tzt6 branchiosto
17	832	40.9	329	11	Q8BLT2	Q8blt2 mus musculu
18	818	40.2	376	13	Q9PWH1	Q9pwh1 gallus gall
19	800.5	39.3	395	5	Q8WS76	Q8ws76 branchiosto
20	798	39.2	375	5	Q8MPL6	Q8mpl6 platynereis
21	787.5	38.7	365	4	Q8N2E5	Q8n2e5 homo sapien
22	785	38.6	360	11	Q9CZW3	Q9czw3 mus musculu
23	785	38.6	360	11	Q8BRC7	Q8brc7 mus musculu
24	783	38.5	358	13	Q9IAU3	Q9iau3 brachydanio
25	779	38.3	350	13	Q8UW39	Q8uw39 fugu rubrip
26	778	38.2	387	13	Q8AY89	Q8ay89 brachydanio
27	774.5	38.0	385	13	Q98SN7	Q98sn7 gallus gall
28	768.5	37.7	360	11	Q8BM17	Q8bm17 mus musculu
29	768.5	37.7	380	11	Q8VCV6	Q8vcv6 mus musculu
30	768.5	37.7	380	11	Q8BMF9	Q8bmf9 mus musculu
31	767	37.7	250	5	Q27671	Q27671 junonia coe
32	765.5	37.6	370	5	Q8WS75	Q8ws75 branchiosto
33	765.5	37.6	385	13	Q9YGX6	Q9ygx6 gallus gall
34	765	37.5	311	11	Q9QXK5	Q9qzk5 rattus norv
35	764	37.5	315	13	Q9PUI3	Q9pui3 gallus gall
36	759	37.3	267	13	Q8UUT7	Q8uut7 gallus gall
37	756	37.1	381	5	Q8T395	Q8t395 cupiennius
38	749	36.8	372	11	Q91XF5	Q91xf5 mus musculu
39	748.5	36.8	371	5	Q8T8A8	Q8t8a8 halocynthia
40	747.5	36.7	331	5	O96867	O96867 strongyloce
41	741.5	36.4	389	13	P79856	P79856 pleurodeles
42	738	36.2	364	11	Q8C6P4	Q8c6p4 mus musculu
43	737	36.2	360	5	Q9U6V0	Q9u6v0 ciona intes
44	724.5	35.6	349	13	O42258	O42258 xenopus lae
45	720.5	35.4	349	4	Q96H90	Q96h90 homo sapien

ALIGNMENTS

RESULT 1

P79752

ID P79752 PRELIMINARY; PRT; 370 AA.
AC P79752;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Wnt1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetradontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99177347; PubMed=10077531;
 RA Gellner K., Brenner S.;
 RT "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu
 RT rubripes.";
 RL Genome Res. 9:251-258(1999).
 CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
 DR EMBL; AF056116; AAC34388.1; -.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Developmental protein; Glycoprotein.
 SQ SEQUENCE 370 AA; 41050 MW; DE0C18B685CEF6E2 CRC64;

Query Match 78.5%; Score 1598; DB 13; Length 370;
 Best Local Similarity 76.8%; Pred. No. 9.6e-149;
 Matches 232; Conservative 41; Mismatches 42; Indels 2; Gaps 2;

QY	1	ALLPGWVSATLLLLAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLL	64
DB	5	ALLLG-VKAACILLVSSLTGTGAVNNSGRWWGIVNVASSNLLTNSKNVQLVLDPSLALL	63
QY	65	SRKQRRRLRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRET	124
DB	64	SRRQRRRLRQNPGLHAIAAGLHAAIKECKWQFRNRRWNCPTTHSPAVFGKIVNRGCRET	123
QY	125	AFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFREF	184
DB	124	AFVFAIMSAGVTHAVARSCSEGAIEFCTCDYRRRGPGGPDWHWGGCSDNVEFGRMFSREF	183
QY	135	VDSGEKGRDLRFLMNLHNEAGRRTTVFSEMRQECKCHGMSGSGCTVRTCWMRLPTLRAVGD	244
DB	134	VDSSERGRDLRYLTNLHNEAGRMTVSSEMRQECKCHGMSGSGCTVRTCWMRLPSFRMVGD	243
QY	245	VLRDRFDGASRVLYGNRGSNRAS-RAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSG	303
DB	244	FLKDRFDGASRVVYANKGSNRASHRAHPRHLEPENPAHKPPSSMDLVYFEKSPNFCSYSG	303
QY	304	RLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCFTHWCCHVSCRNCTHT	363
DB	304	KTGTIGTSGRACNSTSPGLDGCELLCCGRGFKTRTESMTERCHCTFWCCHVSCNCTST	363
QY	364	RVLHECL	370

RESULT 3

Q9GRA6

ID Q9GRA6 PRELIMINARY; PRT; 394 AA.
AC Q9GRA6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Wingless protein.
GN WG.
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461145; PubMed=11003837;
RA Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H.,
RA Yoshioka H., Noji S.;
RT "Correlation of diversity of leg morphology in Gryllus bimaculatus
RT (cricket) with divergence in dpp expression pattern during leg
RT development.";
RL Development 127:4373-4381(2000).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
DR EMBL; AB044713; BAB19660.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 394 AA; 43650 MW; CA2FBF1D505DDAA0 CRC64;

Query Match 56.5%; Score 1151; DB 5; Length 394;
Best Local Similarity 57.0%; Pred. No. 1.1e-104;
Matches 219; Conservative 45; Mismatches 90; Indels 30; Gaps 8;

QY 15 LLLALAALPAALAA--SSGR--WWGIVNVASSTNLLTDSKSLQLVLEPSLQ-LLSRK 67
||:||||| | | | | || | || | : : | ::||: | ||
Db 11 LLMALAGLAARAATRAKMSRGRGSKWGGIAKAGEPNLLPLAPG-ELYMDPAVHATLRRK 69
QY 68 QRRLLRQNPGLHLSVSGGLQSAVRECKWQFRNRRWNCPTA--PGPHLFGKIVNRGCRET 124
||||:| :||:| :| | :| :||:||||||| | | :|||||:|||||
Db 70 QRRLVDRHPGVLLAVVKGANQAIGECQFQFRNRRWNCSTKNFFRGKNLFGKIVDRGCRET 129
QY 125 AFIFAITSAGVTHSVARSCSEGSIESCTCDYRR-----RGPGG-----PDWHWGGCSD 172
|||:|||||:||||:||||:||||:||||| | | | || |||||
Db 130 AFIYAITSAVTHAIARACAEGSIQSCCTCDYRHAGRVAGGRGGGGGGGKPKDWEWGGCSD 189

Qy	173	NIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRITTVFSEMRQECKCHGMSGSGCTVRTC	232
		: : : : :	
Db	190	NIEYGFKFSRDFVDLTGERGRTLREKMNLHNNEAGRLHVREEMRKECKCHGMSGSGCTVKTC	249
Qy	233	WMRLPTLRAVGDLRLDRFDGASRVLYGNRGSNRASRAEL-----LRLEPEDPAHKPPS	285
		: : :	
Db	250	WMRLPHFRVVGDLNLKDRFDGASRVLVGNAGSPRPGGAGKGKGNRYNFQLQPYDAQHKPPG	309
Qy	286	PHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERC	345
		: : : : : : : :	
Db	310	RKDLVYLDQSPNFCERNPRQGIQGTHTGRECNETSLGLDGCIDLCCGRGHRSQEVMLVERC	369
Qy	346	NCTFHWCCHVSCRNCTHTRVLHEC	369
		: : : :	
Db	370	HCTFHWCCFEVKCKTCHVRKTIHTC	393

Q8T'396

QY 14 TLLALLAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLE - PSLQL-LSRKQRR 70
 ||| : | | | : | | | : | : : | : | : |||

Db 17 TLLIPAQAKPRHRGQGRGS-RWWSLAFSEPTNLVVDFHRGNSMNDRGPPAPHLPLRKKQRR 75

Qy 71 LIRQNPGLHSVSGGLQSAVRECKWQFRNRWNCPTAP---GPHLFGKIVNRGCRETAFI 127
|:| ||| : :: |:| : |||:|:| | ||||| | :||| | |||||:

Db 76 LVRDNPQAMQAIGRGVKVAISECKYQFKRRWNCPTADHARGKNIFGKIVQRCRETAFL 135

Qy 128 FAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDS 187
:|||||||:|:| || : :| ||||| | | ||||| | | :|||:

Db 136 YAITSAGVTHSLSRACREGLVSTCNCYRRRGPSGLHWEWGGCSDNIDFGAKFSRQFVDA 195

Qy 188 GEKGRDLRFLMNLHNEAGRITTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDVLR 247
|:|:| ||:| ||||| | | ||:| ||||| |||||:| ||| |:

Db 196 SERGKDLRYIMNLHNEAGRAHVIGMRRQCKCHGMSGCTVQTCWMLSPFRTIGDGLK 255

Qy 248 DRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCTYSGRLGT 307
||||||| ||:| | ||: | | |||| | |||| | ||:| |

Db 256 DRFDGASRVLVTNRGNVR--RRALLK--PYHPEHKPPSKKDLVYFENSPPDFCYADPSLGH 311

Qy 308 AGTAGRACNSSSPALDGCCELLCCGRGHRTRTQVTERCNCNCTFWCCCHVSCRNCTHTRVLH 367
: | || || || : ||:|:| |||||:| : ||||| | | : | | :|:

Db 312 SATLGRTCNVSSLGVDGCDLMCCGRGYKSENREEVSRNCNCTFWCCQVECKTCKTKRLVH 371

Qy 368 ECL 370
|||

Db 372 ECL 374

RESULTS

061699

ID 061699 PRELIMINARY; PRT; 377 AA.

AC 061699;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-JAN-1992 (TrEMBLrel. 09, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE AmphiWnt1.

GN WNT1.

OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

GC Branchiostoma.

OX NCBI_TaxID=7739;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20564609; PubMed=11110906;

RA Schubert M., Holland L.Z., Holland N.D., Jacobs D.K.;

RT "A Phylogenetic Tree of the Wnt Genes Based on All Available Full-

RT Length Sequences, Including Five from the Cephalochordate Amphioxus.";

EL Mol. Biol. Evol. 17:1896-1903(2000).

CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

CC EXTRACELLULAR MATRIX (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.

DR EMBL; AF061974; AAC80432.1; -.

DR InterPro; IPR005817; Wnt.

DR InterPro; IPR005816; Wnt_grthfactor.

DR Pfam; PF00110; wnt; 1.

DR PRINTS; PR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1; 1.

DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 377 AA; 42401 MW; E9A65F3C7F9E5ECB CRC64;

Query Match 52.3%; Score 1064.5; DB 5; Length 377;
Best Local Similarity 51.1%; Pred. No. 3.3e-96;
Matches 191; Conservative 60; Mismatches 102; Indels 21; Gaps 6;

```
QY      13 ATLLALLAALPAALANSSGRWWGI---VNVASSTNL---LTDSKSLQLVLEPSLQLLSR 66
      | :| | | :| | | | | | | | | : : :| :| | :|
Db      9 AVVLLFLAVVPVERVHAVIGRWGIASTVAVQEHANMVPGVARKPGSTIMLDPKKHPLNK 68

QY      67 KQRRLIRQNPGILHSVSGGLQS-----AVRECKWQFRNRWNCPTAPGPH---LFGKIV 117
      | | | | | :| :| | | | | | | | | | | | | | :| | :|
Db      69 KQRRLVRRNPG-----DAGEHRDRPMLAIKECHHQFSKWRWNCVPNTSDHVNSVFGNII 123

QY     118 NRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFG 177
      | | | :| | | :| :| | | | | | | | | | | | | | :| | |
Db     124 LRGCTQTAFIYAVMSAAVAHEVGRNCAEGTITCSCDYRSKGPAGEDWEWGGCSDNVEFG 183

QY     178 RLFGREFVDSGEKGRD-LRFLMNLHNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRL 236
      : | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     184 KQFAKQFVDAGEKTKDSVRYLVNMHNNEAGRVAVAENLRRECKCHGMSGCTLKTTCWMRL 243

QY     237 PTLRAVGDVLRDRFDGASRVI.YGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSP 296
      | | | | | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     244 PNFEDVGDLSLKEKFDGASKVAFPDIGNNRGSRAKVTGLVPANSRHKFPTDNDLVYHERSP 303

QY     297 NFCTYSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQVTERCNCTFHWCCCHVS 356
      | | | :| | | | | | | | :| | | | :| :| :| :| :| :| :|
Db     304 NFCRNNPRLGFEGTRGECNVTSRGLDGC DLLCCGRGYATRQEVTKERCNCTFQWCCQVK 363

QY     357 CRNCTHTRVLHECL 370
      | | | :| :| | |
Db     364 CEECVRTKTIHTCL 377
```

RESULT 6

Q8MPL8

ID Q8MPL8 PRELIMINARY; PRT; 358 AA.
AC Q8MPL8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Wnt1 protein (Fragment).
GN WNT1.
OS Platynereis dumerilii (Dumeril's clam worm).
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllodocida; Nereididae; Platynereis.
OX NCBI_TaxID=6359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182518; PubMed=12194820;
RA Prud'homme B., Lartillot N., Balavoine G., Adoutte A., Vervoort M.;
RT "Phylogenetic analysis of the Wnt gene family: insights from
RT lophotrochozoan members.";
RL Curr. Biol. 12:1395-1400 (2002).

Query Match: 50.9%; Score 1037; DB 5; Length 358;
Best Local Similarity 56.2%; Pred. No. 1.6e-93;
Matches 198; Conservative 42; Mismatches 92; Indels 20; Gaps 5;

RESULT 7
Q8MOP9

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ID      Q8MQP9          PRELIMINARY;          PRT;    468 AA.
AC      Q8MQP9;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      RE02607p.
GN      WG OR CG4889.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Berkeley;
RA      Stapleton M., Brokstein P., Honq L., Aqbayani A., Carlson J.

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RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanenvong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUL-2002) to the EMEL/GenBank/DBJ databases.
 DR EMBL; AY128458; AAM75051.1; -.
 DR FlyBase; FBgn0004009; wg.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 2.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 SQ SEQUENCE 468 AA; 51985 MW; F6F0310A70A864E7 CRC64;

Query Match 50.0%; Score 1018.5; DB 5; Length 468;
 Best Local Similarity 45.5%; Pred. No. 1.5e-91;
 Matches 202; Conservative 44; Mismatches 89; Indels 109; Gaps 8;

QY	31	SGR-----WWGIVNVASSTNLLTDSKSLQLVLEPSL-QLLSRKQRRLLIRQNPGIILHSVSG	84
		: : : :: : : : ::	
Db	30	SGRGRGSMWWGIAKVGEPNNI-----TPIMYMDPAIHSTLRRKQRRLLVRDNPVGLGALVK	84
QY	35	GLQSAVRECKWQFRNRRWNCPT---APGPHLFGKIVNRGCRETAFIFAITSAGVTHSVAR	141
		: : : : : : : : :	
	35	GANAIAISKQHQFRNRRWNCSTRNFSRGKNLFGKIVDRGCRETSFIYAITSAAVTHSIAR	144
QY	142	SCSEGSIESCTCDY---RRRGP-----CGPDWHWGGCSDNIDFGRLEFGREFVDSGE	189
		: : : :	
Db	145	ACSEGTIESCTCDYSHQSRSPQANHQAQSVAGVRDWEWGGCSDNIGFGFKFSREFVDTE	204
QY	190	KGRDLRFLMNLHNEAGRRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLRDR	249
		: : : : : :	
Db	205	RGRNLRKMNHLHNEAGRAHVQAEMRQECKCHGMSGCTVKTWCWMLANFRVIGDNLKAR	264
QY	250	FDGASRVLYGN-----RGSNRASRAELL-----	272
		: :	
Db	265	FDGATRQVQVNSLRATNALAPVSPNAAGSNSVGSNGLIIPQSGLVYEEEEERMLNDHMPD	324
QY	273	-----RLEPEDPAHKPPSP	286
		: :	
Db	325	ILLENSHPISKIHHNMPSPNSLPQAGQRRGRNGRRQGRKHNRHYFQLNPHNPEHKPPGS	384
QY	287	HDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCN	346
		: : : : : :	
Db	385	KDLVYLEPSPSFCEKNLRQILGTHGRQCNETSLGVDGCGLMCCGRGYRRDEVVVVERCA	444
QY	347	CTFHCCHVSCRNCTHTRVLHECL	370
		: : :	
Db	445	CTFHCCEVKCKLCRTKKVIYTCL	468

RESULT 8

Q8MZJ5

ID Q8MZJ5 PRELIMINARY; PRT; 337 AA.
 AC Q8MZJ5;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Wingless (Fragment).
 GN WG.
 OS Pheidole morrisi.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Myrmicinae; Pheidole.
 OX NCBI_TaxID=195110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Abouheif E., Wray G.A.;
 RT "Evolution of the Gene Network Underlying Wing Polyphenism in Ants."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY101369; AAM33135.1; -.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 2.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 FT NON_TER 1 1
 FT NON_TER 337 337
 SQ SEQUENCE 337 AA; 37747 MW; E0DA2498758F33CF CRC64;

Query Match 48.9%; Score 996.5; DB 5; Length 337;
 Best Local Similarity 58.6%; Pred. No. 1.4e-89;
 Matches 188; Conservative 35; Mismatches 59; Indels 29; Gaps 4;

Qy 57 LEPSLQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPT---APGPHLF 113
 :|| | ||||| |:|:| :|| | :| :|:| ||||| | :||
 Db 17 MEPVYATLRRKQRIARENPGVLMASRGANQAIACQYQFRNRRWNCSTKNFLKGKNLF 76
 Qy 114 GKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGP---DWHWGGC 170
 ||||:|||||||:|||| ||||:|:|||||:|:| | : ||||
 Db 77 GKIVDRGCRETAFIYAITSAAVTHSIARACSEGSIQSCSCDYTHQSHASSAVRDWEWGGC 136
 Qy 171 SDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCTVR 230
 ||||:| | |||||:|:|:| ||||| | ||||| ||||| ||||| :
 Db 137 SDNIGYGFKFSREFVDTGERGRNLREKMNHLHNNEAGRAHVTSEMRQECKCHGMSGSCTVK 196
 Qy 231 TCWMRLPTLRAVGDVLRDRFDGASRVLYGNRG-----SNRASRA----- 269
 ||||| | || |:| |||||: | || | :
 Db 197 TCWMRLPNFRVVDNLKDRFDGASRVMSNSDRARVNNNAITSNSASNSVHQHREGLGRR 256
 Qy 270 --ELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCEL 327
 :|:| :| |||| |||| | || | :|:| || || | :| :||:|
 Db 257 QRYNFQLKPYNPEHKPPGQKDLVYVEPSPPFCEKNPKLGILGTYGRQCNDTSIGVDGCDL 316
 Qy 328 LCCGRGHRTRTQRVTERCNCT 348
 :|||||:| | ||:|
 Db 317 MCCGRGHKTQEVTVIERCSCT 337

ID Q8IPI1 PRELIMINARY; PRT; 415 AA.
 AC Q8IPI1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG4889-PB.
 GN WG.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ball   R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan F., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanenvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003617; AAN10628.1; -
 SQ SEQUENCE 415 AA; 46329 MW; 6220D909225E393A CRC64;

Query Match 48.6%; Score 990.5; DB 5; Length 415;
 Best Local Similarity 46.7%; Pred. No. 7.2e-89;
 Matches 194; Conservative 41; Mismatches 81; Indels 99; Gaps 6;

QY 55 LVLEPSL-QLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPT---APGP 110
 : ::||: | |||||:| |||:| :: | : ||: ||||| | : |
 Db 1 MYMDPAIHSTLRRKQRRLLVRDNPGLVKGALVKGANLAISECQHQFRNRRWNCSTRNFSRGK 60
 QY 111 HLFQKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDY--RRRG----- 160
 : |||||: |||||: ||: |||| | |||: ||: ||||: ||||| | : | |
 Db 61 NLFGKIVDRGCRETSFIYAITSAAVTHSIARACSEGTIESCTCDYSHQSRSPQANHQAQS 120
 QY 161 --GGPDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQEC 218
 | || ||||| || | |||||: ||: ||: || ||||| | : |||||
 Db 121 VAGVRDWEWGGCSDNIGFGFKFSREFVDTGERGRNLRKMNHLHNNEAGRAHVQAEMRQEC 180
 QY 219 KCHGMSGCTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGN-----RGS 263
 ||||| |||||: ||||| | : || | : ||||: || | ||
 Db 181 KCHGMSGCTVKTCWMRLANFRVIGDNLKARFDGATRVQVTNSLRATNALAPVSPNAAGS 240
 QY 264 NRASRAELL----- 272
 | :

Db 241 NSVGSNGLIIPQSGLVYGEERMLNDHMPDILLENSHPISKIHHPNMPSNSLPQAGQR 300

Qy 273 -----RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRAC 315
 :| | :| ||| | ||| | ||:| | :| | ||| |

Db 301 GGRNGRRQGRKHNRHYHFQLNPHNPEHKPPGSKDLVYLEPSPSFCEKNLRQGILGTHGRQC 360

Qy 315 NSSSPALDGCCELLCCGRGHRTRTQRVTERCCTFWHCCHVSCRNCTHTRVLHECL 370
 | :| :||| | :||| | :| | ||| | ||| | :| | :| :| |

Db 361 NETSLGVDGCGLMCCGRGYRDEVVVVERCACTFWHCCEVKCKLCRTKKVIYTCL 415

RESULT 10

Q8MZJ2

ID Q8MZJ2 PRELIMINARY; PRT; 334 AA.

AC Q8MZJ2;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Wingless (Fragment).

GN WG.

OS Formica nitidiventris.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;

OC Formicinae; Formica.

OX NCBI_TaxID=195149;

RN [1]

RP SEQUENCE FROM N.A.

RA Abouheif E., Wray G.A.;

RT "Evolution of the Gene Network Underlying Wing Polyphenism in Ants.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY101372; AAM33138.1; -.

DR InterPro; IPR005817; Wnt.

DR InterPro; IPR005816; Wnt_grthfactor.

DR Pfam; PF00110; wnt; 2.

DR PRINTS; PR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1; 1.

DR PROSITE; PS00246; WNT1; 1.

FT NON_TER 1 1

FT NON_TER 334 334

SQ SEQUENCE 334 AA; 37495 MW; 58D094810D4A432B CRC64;

Query Match 48.6%; Score 989; DB 5; Length 334;

Best Local Similarity 60.3%; Pred. No. 7.6e-89;

Matches 187; Conservative 35; Mismatches 62; Indels 26; Gaps 4;

Qy 64 LSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRWNCPT---APGPHLFGKIVNRG 120
 | |||||:|:|:| | :| | |||: ||||| | | :|||:|:

Db 24 LRRKQRRLLVRENPGLQAVARGANQVAECQHQFRNRWNCSTKNFLRGKLNFGKIVDKG 83

Qy 121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDY---RRRGPGGPDWHWGGCSDNIDFG 177
 |||||:|||| | |||:|:|||||:|:| | ||| | |

Db 64 CRETAFIYAITSAAVIHSIARACSEGSIQSCSCDYTHQSRSSAVRDWEWGGCSDNIGYG 143

Qy 178 RLFGREFVDSGEKGRDLRFLMNLHNEAGRRTTVFSEMRQECKCHGMSGCTVRTCWMRLP 237
 | ||||:|:|:| | ||||| | ||||| | ||||| | ||||| |

Db 144 FKFSREFVDTGERGRNLREKMNHLHNEAGRTHVSSEMRQECKCHGMSGCTVKTTCWMRLP 203

Qy 238 TLRAVGDVLRDRFDGASRVLYGNRGSNRAS-----RAELLR-----LEPE 277
 : | | | | : | | | | | | : | | : | | | : |
 Db 294 SFRVVGDNLDKDRFDGASRVMSNSDRVRSNVHVNSASNSVHQHRDGLARRQRYNFQLKPY 263
 Qy 273 DPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTR 337
 : | | | | | | | | : | | | : | | | | | | : | : | | | : | | | : | |
 Db 264 NPEHKPPGPKDLVYLEQSPAFCEKNPALGILGTHGRQCNDTSLGVDGCDLMCCGRGYKTQ 323
 Qy 338 TQRVTERCNC 347
 | | | | |
 Db 324 EVVVIERCNC 333

RESULT 11

Q8MZJ4

ID Q8MZJ4 PRELIMINARY; PRT; 337 AA.
 AC Q8MZJ4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Wingless (Fragment).
 GN WG.
 OS Crematogaster lineolata.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Myrmicinae; Crematogaster.
 OR NCBI_TaxID=195111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Abouheif E., Wray G.A.;
 RT "Evolution of the Gene Network Underlying Wing Polyphenism in Ants.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY101370; AAM33136.1; -.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 2.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 FT NON_TER 1 1
 FT NON_TER 337 337
 SQ SEQUENCE 337 AA; 37863 MW; 6462D40582CB4274 CRC64;

Query Match 47.7%; Score 971; DB 5; Length 337;
 Best Local Similarity 57.1%; Pred. No. 4.6e-87;
 Matches 190; Conservative 34; Mismatches 79; Indels 30; Gaps 5;

Qy 45 NLLTDSKSLQLVLEPSLQLLSRKQRRLLIRONPGILHSVSGGLQSAVRECKWQFRNRRWNC 104
 | | | | : : | | | | : | | : | | : | | | | |
 Db 65 NFLPMSAS-SIHMERFYATLRRKQRRLLAIENPGVLMASRGANQAIAECQHQRNRRWNC 64
 Qy 105 PT---APGPHLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDY---RRR 158
 | : | | | | | | | | | | | | | | | | | | : | | | | |
 Db 65 STKNFLRGKNLFGKIVDRGCRETAFIYAITSAAVTHSIARACSEGSIQLCSCDYTHQSRA 124
 Qy 159 GPGGPDWHWGGCSDNIDFGRILFGREFVDSGEKGRDLRFLMNLHNNEAGRITTVFSEMROEC 218
 | | | | | | | | : | | | | | : | | : | | | | | | | | | | |

Db 125 SSAVRDWEWGGCSDNIGYGFKFSREFVDTGERGRNLREKMNHLHNEAGRAHVTSEMRQEC 184

QY 219 KCHGMSGSCVTVRTCWMRLPTLRAVGDLRDRFDGASRVLYGN----RGSNRASRAEL--- 271
 |||||:||||| | ||| |:|||||: | ||| :
 Db 185 KCHGMSGSCVTKTCWMRLPNFRLVGDNLKDRFDGASRVMSNSDRVRVSNNAITSNSASN 244

QY 272 -----LRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRAC 315
 :|:| :| ||| |||| | || | : :|| || ||
 Db 245 SVHQHRDGLGRRHRYNFQLKPYNPEHKPPGQKDLVYVEPSPPFCEKNPKLGILGTQGRQC 304

QY 316 NSSSPALDGCCELLCCGRGHRTRTQRVTERCNCT 348
 | :| :|||:|:|||||:|: | |||:|
 Db 305 NDTSIGVDGCDLMCCGRGHKTQEVTVIERCSCT 337

RESULT 12

Q8MZJ3

ID Q8MZJ3 PRELIMINARY; PRT; 330 AA.
 AC Q8MZJ3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Wingless (Fragment).
 CN WG.
 OS Myrmica americana.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Myrmicinae; Myrmica.
 CC NCBI_TaxID=195148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Abcuheif E., Wray G.A.;
 RT "Evolution of the Gene Network Underlying Wing Polyphenism in Ants."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY101371; AAM33137.1; -.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 2.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 FT NON_TER 1 1
 FT NON_TER 330 330
 SQ SEQUENCE 330 AA; 37034 MW; 737B23B0426E39DF CRC64;

Query Match 46.7%; Score 950.5; DB 5; Length 330;
 Best Local Similarity 55.6%; Pred. No. 4.6e-85;
 Matches 184; Conservative 36; Mismatches 80; Indels 31; Gaps 5;

QY 41 ASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLRQNPGLHSVSGGLQSAVRECKWQFRNR 100
 | | : : :| | |||:| | |||:| :|:| | :|:| ||||
 Db 1 AGEPNNFLPMSAASIHMEPIYTLRRKQKRLARDNPGVLMVARGANQAITECQHQFRNR 60

QY 101 RWNCP---APGPHLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDY-- 155
 |||| | | :|||||:|||||:| || ||||:|:|||||:|:|
 Db 61 RWNCKTNFLRGKNLFGKIVDRGCRETAFVYAIASAAVTHSIARACSEGSIQSCSCDYTH 120

QY 156 -RRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEM 214
 Db 121 QSRASSAVRDWEWGGCSDNIGYGFKFSREFVDTERGRNLRKMNHLHNNEAGRAHVTSEM 180
 QY 215 RQECKCHGMSGSCVTRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRG-----SN 264
 Db 181 RQECKCHGMSGSCVKTCTWMRLPNFRVVGDNLKDRFDGASRVVMVSNDRVRVNNNAIMSN 240
 QY 265 RASRA-----ELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTA 311
 Db 241 SASNSVHQHREGLGRRHRYNFQLKPYNPEHKPPGQKDLVYVEQSPPFCEKNPKLGILGTH 300
 QY 312 GRACNSSSPALDGCELLCCGRGHRTRTQRTV 342
 Db 301 GRQCNDTSIGVDGCDLMCCGRGH--KTQEV 329

RESULT 13

Q8WRF7

ID Q8WRF7 PRELIMINARY; PRT; 365 AA.
 AC Q8WRF7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Signaling protein wingless (Fragment).
 GN WG.
 OS Mysidium columbiae.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Peracarida; Mysidacea; Mysida; Mysidae; Mysidium.
 NX NCBI_TaxID:178358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duman-Scheel M., Pirkel N., Patel N.H.;
 RT "Analysis of the expression pattern of Mysidium columbiae wingless
 RT provides evidence for conserved mesodermal and retinal patterning
 RT processes among insects and crustaceans."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
 DR EMBL; AF438206; AAL37756.1; .
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Developmental protein; Glycoprotein.
 FT NON_TER 365 365
 SQ SEQUENCE 365 AA; 41260 MW; 45624F91143D4EA1 CRC64;

Query Match 43.1%; Score 878.5; DB 5; Length 365;
 Best Local Similarity 45.9%; Pred. No. 6.5e-78;
 Matches 159; Conservative 62; Mismatches 106; Indels 31; Gaps 6;

QY 7 LPGWVSATLLIALAALPAALANSSGR-----WWGIVNVASSTNL-----LTD\$KSLQL 55

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      :|  |  :| :|||  |  :  |  ||  :  :||  |::|  |
Db      1 MPAPKGAAFVL-IAALACAFVCEAQARKYKGPKWWNLGLSVDPSNLSNEILSNLSLSDHH 59

Qy      56 VLEPSLQLLSRKQRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTA-----PGP 110
      :  |  ::| :||| |||:| |::| :| :  | :| :||| |||:|  :
Db      60 LSESVQRMRLRKQRRLIRENDGVLVAIAEGAKKAASKCRYQFRSRRWDCSASRKKKIKRR 119

Qy      111 HLF GKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGC 170
      |||:|:| :||| |||:|:| || | ||| |::|:|:| ||:| |  :  | || |||
Db      120 RLFGRIVSIPCRETAFVYALLSAAVLHSVTRACTEGAVHSCSCHYTAK---GDDWEWGGC 176

Qy      171 SDNIDFGRLFGRFVDSGEKGRDLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGSCTVR 230
      |:||||| | | |||:||| :::| ||| ||| ||| ||| ||| :|
Db      177 SENIDFGYRFSRHFVDAGEKTHEIRAAMNLHNNEAGRQHVRAAMRSECKCHGMSGSCTVK 236

Qy      231 TCWMRLPTRLRAVGDLRDRFDGASRVL-----YGNRGSNRASRAELLRLEPEDP 279
      ||| ||| : :|| |::| ||| ||| :| :| :| :| :| :|
Db      237 TCWSRLPHFKQIGDRLKEKFDGASRVMSRHTAHMQRRSNSRRRSIKRKRKNLQPYNP 296

Qy      280 AHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQ 339
      || || ||| :||| ||| : || ||| :| || :| :|| |::| ||| :|
Db      297 DHKSPSAMDVLVYLQESPNFCVRNRTLGIPTSERECNGTSIGVEGCNLMCCGRGYSSRVV 356

Qy      340 RVTERCNC 347
      | |||:|
Db      357 EVVERCSC 364

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RESULT 14

Q9TX64

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ID   Q9TX64          PRELIMINARY;          PRT;   303 AA.
AC   Q9TX64;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Wingless product (Fragment).
OS   Tribolium castaneum (Red flour beetle).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC   Tenebrionidae; Tribolium.
OX   NCBI_TaxID=7070;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94150623; PubMed=8107804;
RA   Nagy L.M., Carroll S.;
RT   "Conservation of wingless patterning functions in the short-germ
RT   embryos of Tribolium castaneum.";
RL   Nature 367:460-463(1994).
CC   -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC   EXTRACELLULAR MATRIX (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
DR   InterPro; IPR005817; Wnt.
DR   InterPro; IPR005816; Wnt_grthfactor.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.

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Query Match 41.2%; Score 838; DB 4; Length 351;
 Best Local Similarity 44.8%; Pred. No. 6e-74;
 Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

```

Qy      14 TLLALALPAALAAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLIR 73
      :| | : | : | :| |      | :  ||  : : : :  | : | :| : :
Db      9 SLRLLVFAVFSAAASN-----WLYLAKLSSVGSISEETCE-----KLKGLIQRQVQMCK 58

Qy      74 QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133
      :| : : || | | | : || : || : || : || : || : || : || : ||
Db      59 RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVTTQGTREAAAFVYAISSA 118

Qy     134 GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGR- 192
      || : | : || | : | | | | : | | | | | : | | : || | : :
Db     119 GVAFVTRACSSGELEKCGCDRTVHGVTPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKG 178

Qy     193 --DLRFLMNLHNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDVLRDRF 250
      | | | | | | | | | : : | | | | | : | | | | : | | | | : : |
Db     179 ASSSRALMNLHNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKF 238

Qy     251 DGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310
      ||| : | | : || | : | | : | | | | | | : | | | |
Db     239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT 291

Qy     312 AGRACNSSSPALDGCELLCCGRGHRTTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
      || | | : | : || | | | | | | | : ||| : | | | | | | | | |
Db     292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKRCQCQRLVELHTC 350

```

Search completed: January 21, 2004, 10:48:12
 Job time : 44 secs

OM protein - protein search, using sw model

Run on: January 21, 2004, 10:37:56 ; Search time 17 Seconds
(without alignments)
1023.522 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2036
Sequence: 1 MGLWALLPGWVSATLLLLALA.....WCCHVSCRNCTHTRVLHECL 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	2036	100.0	370	1	WNT1_HUMAN	P04628 homo sapien
2	2021	99.3	370	1	WNT1_MOUSE	P04426 mus musculu
3	1671	82.1	369	1	WNT1_AMBME	P21551 ambystoma m
4	1595	78.3	370	1	WNT1_BRARE	P24257 brachydanio
5	1463	71.9	371	1	WNT1_XENLA	P10108 xenopus lae
6	1063.5	52.2	392	1	WNT1_BOMMO	P49340 bombyx mori
7	1022.5	50.2	468	1	WNTG_DROME	P09615 drosophila
8	843.5	41.4	352	1	WN3A_MOUSE	P27467 mus musculu
9	843.5	41.4	355	1	WNT3_MOUSE	P17553 mus musculu
10	843	41.4	351	1	WNT4_XENLA	P49338 xenopus lae
11	840.5	41.3	355	1	WNT3_HUMAN	P56703 homo sapien
12	840	41.3	351	1	WNT4_HUMAN	P56705 homo sapien
13	836	41.1	351	1	WNT4_MOUSE	P22724 mus musculu
14	836	41.1	351	1	WNT4_RAT	Q9qxx5 rattus norv
15	832	40.9	351	1	WNT4_CHICK	P49337 gallus gall
16	827.5	40.6	352	1	WN3A_HUMAN	P56704 homo sapien
17	822.5	40.4	352	1	WN3A_XENLA	P31285 xenopus lae

18	819.5	40.3	352	1	WN4A_BRARE	P47793	brachydanio
19	815.5	40.1	223	1	WNT1_STRPU	P28094	strongyloce
20	792	38.9	391	1	WN2B_HUMAN	Q93097	homo sapien
21	787.5	38.7	365	1	WNT6_HUMAN	Q9y6f9	homo sapien
22	785	38.6	360	1	WNT2_HUMAN	P09544	homo sapien
23	784	38.5	389	1	WN2B_MOUSE	O70283	mus musculu
24	781	38.4	360	1	WNT2_MOUSE	P21552	mus musculu
25	780.5	38.3	364	1	WNT6_MOUSE	P22727	mus musculu
26	772.5	37.9	351	1	WN2B_XENLA	P87387	xenopus lae
27	772	37.9	379	1	WN5A_RAT	Q9qxq7	rattus norv
28	769	37.8	379	1	WN5A_MOUSE	P22725	mus musculu
29	766.5	37.6	365	1	WN5A_HUMAN	P41221	homo sapien
30	762.5	37.5	371	1	WN5B_ORYLA	O42122	oryzias lat
31	760	37.3	350	1	WNT2_BRARE	Q92048	brachydanio
32	758	37.2	359	1	WN5A_PLEWA	O13267	pleurodeles
33	754.5	37.1	380	1	WN5A_XENLA	P31286	xenopus lae
34	753	37.0	359	1	WN5A_AMBME	Q06442	ambystoma m
35	747	36.7	363	1	WNT5_BRARE	Q92050	brachydanio
36	747	36.7	417	1	WN1A_HUMAN	Q9gzt5	homo sapien
37	743.5	36.5	359	1	WN5B_MOUSE	P22726	mus musculu
38	742.5	36.5	359	1	WN5B_HUMAN	Q9h1j7	homo sapien
39	742	36.4	417	1	WN1A_MOUSE	P70701	mus musculu
40	741	36.4	364	1	WN16_MOUSE	Q9qys1	mus musculu
41	730.5	35.9	365	1	WN16_HUMAN	Q9ubv4	homo sapien
42	729	35.8	363	1	WNT5_HALRO	O15978	halocynthia
43	728.5	35.8	357	1	WN5B_AMBME	Q06443	ambystoma m
44	724.5	35.6	360	1	WN5C_XENLA	P33945	xenopus lae
45	722.5	35.5	442	1	WN1A_BRARE	P43446	brachydanio

ALIGNMENTS

RESULT 1

WNT1_HUMAN

ID WNT1_HUMAN STANDARD; PRT; 370 AA.

AC P04628;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Wnt-1 proto-oncogene protein precursor.

CN WNT1 OR INT1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86055728; PubMed=2998762;

RA van Ooyen A., Kwee V., Nusse R.;

RT "The nucleotide sequence of the human int-1 mammary oncogene;

RT evolutionary conservation of coding and non-coding sequences.";

RL EMBO J. 4:2905-2909(1985).

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN

CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A

CC SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO

CC SIGNAL OVER ONLY FEW CELL DIAMETERS.

Db 241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300

Qy 301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNC'TFHWCC'HVSCRNC 360
 |||

Db 301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNC'TFHWCC'HVSCRNC 360

Qy 361 THTRVLHECL 370
 |||

Db 361 THTRVLHECL 370

RESULT 2

WNT1_MOUSE

ID WNT1_MOUSE STANDARD; PRT; 370 AA.

AC P04426;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Wnt-1 proto-oncogene protein precursor.

GN WNT1 OR WNT-1 OR INT-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H;

RX MEDLINE=85024897; PubMed=5091914;

RA Ooyen A.V., Nusse R.;

RT "Structure and nucleotide sequence of the putative mammary oncogene

int-1; proviral insertions leave the protein-encoding domain

intact.";

RL Cell 39:233-240(1984).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86310810; PubMed=3018519;

RA Fung Y.-K.T., Shackleford G.M., Brown A.M.C., Sanders G.S.,

RA Varmus H.E.;

RT "Nucleotide sequence and expression in vitro of cDNA derived from

mRNA of int-1, a provirally activated mouse mammary oncogene.";

PL Mol. Cell. Biol. 5:3337-3344(1985).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=91122634; PubMed=2279700;

RA Gavin B.J., McMahon J.A., McMahon A.P.;

RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal

and adult mouse development.";

RL Genes Dev. 4:2319-2332(1990).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Czech II;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RP POSSIBLE FUNCTION.

RX MEDLINE=90363290; PubMed=2202907;

RA Thomas K.R., Capecchi M.R.;

RT "Targeted disruption of the murine int-1 proto-oncogene resulting in
RT severe abnormalities in midbrain and cerebellar development.";

RL Nature 346:847-850(1990).

RN [6]

RP DEVELOPMENTAL STAGE.

RC STRAIN=CBA/CA; TISSUE=Embryo;

RX MEDLINE=87244326; PubMed=3594565;

RA Wilkinson D.G., Bales J.A., McMahon A.P.;

RT "Expression of the proto-oncogene int-1 is restricted to specific
RT neural cells in the developing mouse embryo.";

RL Cell 50:79-88(1987).

RN [7]

RP TISSUE SPECIFICITY.

RC STRAIN=ICR;

RX MEDLINE=87244327; PubMed=3594566;

RA Shackelford G.M., Varmus H.E.;

RT "Expression of the proto-oncogene int-1 is restricted to postmeiotic
RT male germ cells and the neural tube of mid-gestational embryos.";

RL Cell 50:89-95(1987).

CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
CC SIGNAL OVER ONLY FEW CELL DIAMETERS. PROEMINENT ROLE IN THE
CC INDUCTION OF THE MESENCEPHALON AND CEREBELLUM. MAY PLAY A CRUCIAL
CC ROLE IN THE MORPHOGENESIS OF THE NEURAL TUBE AND/OR THE EARLY
CC STAGES OF CNS DEVELOPMENT.

CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.

CC -1- TISSUE SPECIFICITY: TESTIS AND MID-GESTATIONAL EMBRYOS. IN THE
CC TESTIS, DETECTED ONLY IN POSTMEIOTIC GERM CELLS UNDERGOING
CC DIFFERENTIATION FROM ROUND SPERMATIDS INTO MATURE SPERMATOZOA. IN
CC THE EMBRYOS, EXPRESSION IS RESTRICTED TO THE DEVELOPING CNS IN
CC REGIONS OF THE NEURAL TUBE OTHER THAN THE TELENCEPHALON.

CC -1- DEVELOPMENTAL STAGE: ACCUMULATES THROUGHOUT THE NEURAL PLATE AT
CC THE ANTERIOR HEAD FOLDS OF THE 9 DAY EMBRYO BUT ONLY AT ITS
CC LATERAL TIPS IN MORE POSTERIOR REGIONS. FOLLOWING NEURAL TUBE
CC CLOSURE, EXPRESSION IS RESTRICTED TO SPECIFIC REGIONS OF THE
CC DORSAL WALL OF THE BRAIN VENTRICLES AND SPINAL CORD, THE VENTRAL

CC WALL OF THE MIDBRAIN AND THE DIENCEPHALON, AND THE LATERAL WALLS
 CC OF THE NEUROEPITHELIUM AT THE MIDBRAIN-HINDBRAIN JUNCTION.
 CC -!- DISEASE: MANY MOUSE MAMMARY TUMORS INDUCED BY MOUSE MAMMARY TUMOR
 CC VIRUS (MMTV) CONTAIN A PROVIRUS INTEGRATED INTO A HOST CELL REGION
 CC WHICH HAS BEEN NAMED INT-1 (NOW WNT-1).
 CC -!- SIMILARITY: Belongs to the Wnt family.

CC -----
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 CC -----

DR EMBL; K02593; AAA39321.1; -.
 DR EMBL; M11943; AAA39322.1; -.
 DR EMBL; BC005449; AAH05449.1; -.
 DR PIR; A23447; TVMST1.
 DR MGD; MGI:98953; Wnt1.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Wnt signaling pathway; Developmental protein; Proto-oncogene;
 KW Glycoprotein; Signal.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 370 WNT-1 PROTO-ONCOGENE PROTEIN.
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 370 AA; 41085 MW; 02EEB23109231A40 CRC64;

Query Match 99.3%; Score 2021; DB 1; Length 370;
 Best Local Similarity 98.9%; Pred. No. 1.9e-169;
 Matches 366; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGLWALLPGWVSATLLALLAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60
 ||||| : |||||
 Db 1 MGLWALLPSWVSTTLLALTALPAALAANSSGRWWGIVNIASSTNLLTDSKSLQLVLEPS 60
 QY 61 LQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
 ||||| : |||||
 Db 61 LQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
 QY 121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGCSNIDFGRLF 180
 ||||| : |||||
 Db 121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGCSNIDFGRLF 180
 QY 181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240
 ||||| : |||||
 Db 181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240
 QY 241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300

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Db      241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT 300
QY      301 YSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360
Db      301 YSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360
QY      361 THTRVLHECL 370
Db      361 THTRVLHECL 370

```

RESULT 3

WNT1_AMBME

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ID      WNT1_AMBME      STANDARD;      PRT;      369 AA.
AC      P21551;
DT      01-MAY-1991 (Rel. 18, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Wnt-1 protein precursor.
GN      WNT-1.
OS      Ambystoma mexicanum (Axolotl).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC      Ambystoma.
OX      NCBI_TaxID=8296;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91081334; PubMed=2259633;
RA      Busse U., Guay J., Seguin C.;
RT      "Nucleotide sequence of a cDNA encoding Wnt-1 of the Mexican axolotl
RT      Ambystoma mexicanum.";
RL      Nucleic Acids Res. 18:7439-7439(1990).
RN      [2]
RP      ERRATUM.
RX      MEDLINE=91204483; PubMed=2017393;
RA      Busse U., Guay J., Seguin C.;
RL      Nucleic Acids Res. 19:981-981(1991).
RN      [3]
RP      CHARACTERIZATION.
RX      MEDLINE=93285407; PubMed=8508949;
PA      Busse U., Seguin C.;
RT      "Molecular analysis of the Wnt-1 proto-oncogene in Ambystoma
RT      mexicanum (axolotl) embryos.";
RL      Differentiation 53:7-15(1993).
CC      -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC      TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC      SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
CC      SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC      -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC      extracellular matrix.
CC      -!- DEVELOPMENTAL STAGE: EARLY BLASTULA UNTIL GASTRULATION, BARELY
CC      EXPRESSED DURING GASTRULATION AND PRESENT AGAIN FROM NEURULATION
CC      UNTIL LATE EMBRYOGENESIS.
CC      -!- SIMILARITY: Belongs to the Wnt family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration

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DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Wnt-1 protein precursor.
 GN WNT1 OR WNT-1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184125; PubMed=2009859;
 RA Molven A.; Njolstad P.R.; Fjose A.;
 RT "Genomic structure and restricted neural expression of the zebrafish
 RT wnt-1 (int-1) gene.";
 RL EMBO J. 10:799-807(1991).
 CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
 CC SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
 CC SIGNAL OVER ONLY FEW CELL DIAMETERS.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix.
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC -----
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 CC -----
 DR EMBL; X58880; CAA41687.1; -.
 DR EMBL; X58881; CAA41687.1; JOINED.
 DR EMBL; X58882; CAA41687.1; JOINED.
 DR EMBL; X58883; CAA41687.1; JOINED.
 DR PIR; S15013; S15013.
 DR ZFIN; ZDB-GENE-980526-526; wnt1.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 370 WNT-1 PROTEIN.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CQ SEQUENCE 370 AA; 41010 MW; F2AB0A82DB031D3E CRC64;

Query Match 78.3%; Score 1595; DB 1; Length 370;
 Best Local Similarity 75.7%; Pred. No. 3.6e-132;
 Matches 281; Conservative 47; Mismatches 41; Indels 2; Gaps 2;

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
 CC SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
 CC SIGNAL OVER ONLY FEW CELL DIAMETERS.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix.
 CC -!- TISSUE SPECIFICITY: AT NEURULA IN ANTERIOR NEURAL FOLD; AT TAILBUD
 CC IN DORSAL MIDLINE OF MIDBRAIN.
 CC -!- DEVELOPMENTAL STAGE: NEURULA ONWARDS.
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC -----
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 CC -----
 DR EMBL; X13138; CAA31528.1; -.
 DR PIR; S02113; TVXLTL.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 371 WNT-1 PROTEIN.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 371 AA; 41125 MW; 1FACE4F5F0CB4B72 CRC64;

Query Match 71.9%; Score 1463; DB 1; Length 371;
 Best Local Similarity 70.0%; Pred. No. 1.3e-120;
 Matches 261; Conservative 50; Mismatches 50; Indels 12; Gaps 5;

QY 1 MGLWALLPGWVSATLLALLAALPAALAANSSGRWWGIVNVASSTNLL--TDSKSLQLVLE 58
 :|| | || || :|| :| :|||:|||||||: || :|| :||: |||:
 Db 8 LGLKTL---WV-----LAFSSLSNTIAVNNSGKWWGIVNVASAGNVLPGSDARPVPLVLD 59
 QY 59 PSLQLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIYN 118
 ||||| | :||||||| | :| || :||| | ||||| | | :||| :|
 Db 60 PSLQLLSR-QKRLIRQNPGLQSITRGLHSAIRECKWHFRNRRWNCPTGTGNQVFGKIIN 118
 QY 119 RGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGR 178
 ||||| | :||||||| | ||||| | :||| | ||||| | ||||| | :|||
 Db 119 RGCRETAFVFAITSAGVTHSVARSCSEGSIESCSCDYRRRGPGGPDWHWGGCSDNIEFGR 178
 QY 179 LFGREFVDSGEKGRDLRFLMNLHNNAGRTTVFSEMRQECKCHGMSGSCVTRTCWMRLPT 238
 ||||| | | :||| :| :||| :|| | || :||| | ||||| | :|||
 Db 179 FIGREFVDSSERGRDLKYLVLNHLNNQAGRLTVLTEMRECKCHGMSGCSLRTCWMRLPP 238
 QY 239 LRAVGDVLRDRFDGASRVLYGNRGSNR-ASRAELLRLEPEDPAHKPPSPHDLVYFEKSPN 297

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Db      239 FRSVGDALKDRFDGASKVTYSNNGSNRWGSRSDPPHLEPENPTHALPSSQDLVYFEKSPN 298
QY      298 FCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSC 357
      ||: | : || || || || ||: | ||||| |||||:| | || ||||| |||||
Db      299 FCSPSEKNGTPGTTGRICNSTSLGLDGCELLCCGRGYRSLAEKVTERCHCTFNWCCHVTC 358
QY      358 RNCTHTRVLHECL 370
      ||| ::::|||
Db      359 LNCTSSQIVHECL 371

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RESULT 6

WNT1_BOMMO

```

ID WNT1_BOMMO STANDARD; PRT; 392 AA.
AC P49340;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Wnt-1 protein precursor.
GN WNT-1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
EN [1]
RP SEQUENCE FROM N.A.
RA Amanai K., Hui C., Kokubo H., Ueno K., Suzuki Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS.
CC !- SUBCELLULAR LOCATION: Secreted (Probable)
CC !- SIMILARITY: Belongs to the Wnt family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D14169; BAA03211.1; -.
DR EnterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 392 WNT-1 PROTEIN.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 392 AA; 44204 MW; EE25BFE2810F44D6 CRC64;

```

Query Match 52.2%; Score 1063.5; DB 1; Length 392;
 Best Local Similarity 56.3%; Pred. No. 1.2e-85;
 Matches 205; Conservative 39; Mismatches 91; Indels 29; Gaps 8;

```

QY      34 WWGIVNVASSTNLLTDSKSLQLVLEPSLQ-LLSRKQRRLLRQNPGLHSVSGGLQSAVRE 92
      ||||  ||  | : | ::||  ||||| | :||| : | : | ||  |
Db      31 WWGIAKAGEPNNLSPVSPGV-LFMDPAVHATLRRKQRRLLARENPGVLA AVAKA-QYAF AE 88

QY      93 CKWQFRNRRWNCPT---APGPHLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIE 149
      | : || : ||||| |  | : ||||| : ||||| : ||||| : ||| : |||
Db      89 CQHQFKYRRWNCSTRNFLRGKNLFGKIVDRGCRETAFIYAIT SAGVTHSLARACREASIE 148

QY     150 SCTCDYRRR-----GPGGPD-----WHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMN 199
      ||||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     149 SCTCDYSHRPRAAQNPVGGRANVRVWKWGGCSDNIGFGFRFSREFVDTGERGKTLREKMN 208

QY     200 LHNNEAGRTTVFSEMRQECKCHGMSG SCTVRTCWMRLPTLRAVGDVLRDRFDGASRVLY- 258
      ||||| |  | : || : ||||| : ||||| : ||||| : ||| : ||||| : |||
Db     209 LHNNEAGRPHVQTEMKQECKCHGMSG SCTVKT CWMRLPSFR.SVGDSLKDRFDGASRVMLS 268

QY     259 -----GNRGSNRRASRAELLR--LEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLG 306
      : | | : | | | : | | | |  |  |  |  |  |  |  |  |  |  |
Db     269 KADVETPAQRNEAAPHRVPRKDRYRFQLRPHNPDHKSPGVKDLVYLESSPGFCEKNPRLG 328

QY     307 TAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRTVCNCTFHWCCHVSCRNCIHTRVL 366
      || ||||| : | : ||| : ||||| : ||| |  |  |  |  |  |  |  |  |  |  |
Db     329 IPETHGRACNDTSIGVDGCDLMCCGRGYKTNTMFVVERCNCTFHWCCCEVKCKLCRTEKVV 388

QY     357 HECL 370
      |  |  |
Db     389 HTCL 392
  
```

RESULT 7

WNTG_DROME

ID WNTG_DROME STANDARD; PRT; 468 AA.
 AC P09615; Q27768; Q27769; Q9VM27;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein int-1 precursor (dInt-1) (Wingless protein).
 GN WG OR CG4889.
 QS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87273528; PubMed=3111720;
 FA Rijsewijk F., Schuermann M., Wagenaar E., Parren P., Weigel D.,
 FA Nusse R.;
 RT "The Drosophila homolog of the mouse mammary oncogene int-1 is
 RT identical to the segment polarity gene wingless.";
 RL Cell 50:649-657(1987).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88203634; PubMed=3129722;
 RA Uzvoelgyi E., Kiss I., Pitt A., Arsenian S., Ingvarsson S.,
 RA Udvardy A., Hamada M., Klein G., Suemegi J.;
 RT "Drosophila homolog of the murine Int-1 protooncogene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3034-3038(1988).
 RN [3]
 RP SEQUENCE FROM N.A., AND MUTANTS.
 RX MEDLINE=94085405; PubMed=8262072;
 RA van den Heuvel M., Harryman-Samos C., Klingensmith J., Perrimon N.,
 RA Nusse R.;
 RT "Mutations in the segment polarity genes wingless and porcupine
 RT impair secretion of the wingless protein.";
 RL EMBO J. 12:5293-5302(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., McBarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [5]

RP SECRETION.
 RX MEDLINE=90058657; PubMed=2582493;
 RA van den Heuvel M., Nusse R., Johnston P., Lawrence P.A.;
 RT "Distribution of the wingless gene product in Drosophila embryos: a
 RT protein involved in cell-cell communication.";
 RL Cell 59:739-749(1989).
 RN [6]
 RP PHOSPHORYLATION OF ARM.
 RX MEDLINE=95113174; PubMed=7529201;
 RA Peifer M., Pai L.M., Casey M.;
 RT "Phosphorylation of the Drosophila adherens junction protein
 RT Armadillo: roles for wingless signal and zeste-white 3 kinase.";
 RL Dev. Biol. 166:543-556(1994).
 RN [7]
 RP INTERACTION WITH WG AND EN.
 RC TISSUE=Embryo;
 RX MEDLINE=93113685; PubMed=1335365;
 RA Siegfried E., Chou T.B., Perrimon N.;
 RT "wingless signaling acts through zeste-white 3, the Drosophila homolog
 RT of glycogen synthase kinase-3, to regulate engrailed and establish
 RT cell fate.";
 RL Cell 71:1167-1179(1992).
 CC -!- FUNCTION: Segment polarity protein. Binds to the frizzled seven-
 CC transmembrane receptors. This protein is probably a growth factor.
 CC Acts on neighboring cells to regulate at least one gene, the
 CC homeobox segmentation gene engrailed. Wg signal represses arm
 CC phosphorylation. Wg signaling operates by inactivating the sgg
 CC repression of engrailed autoactivation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the Wnt family.

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 DR EMBL; M17230; AAA28647.1; -.
 DR EMBL; J03650; AAA28646.1; -.
 DR EMBL; S67382; AAB29368.1; -.
 DR EMBL; S67383; AAB29369.1; -.
 DR EMBL; AE003617; AAF52501.1; -.
 DR PIR; A29650; A29650.
 DR FlyBase; FBgn0004009; wg.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005110; F:frizzled-2 binding activity; IDA.
 DR GO; GO:0008595; P:determination of anterior/posterior axis, e. . .; NAS.
 DR GO; GO:0008544; P:epidermal differentiation; IMP.
 DR GO; GO:0007223; P:frizzled-2 receptor signaling pathway; IDA.
 DR GO; GO:0007483; P:genital disc metamorphosis; NAS.
 DR GO; GO:0007442; P:hindgut morphogenesis; IMP.
 DR GO; GO:0007560; P:imaginal disc morphogenesis; NAS.
 DR GO; GO:0007523; P:larval visceral muscle development; IMP.
 DR GO; GO:0007479; P:leg disc proximal/distal pattern formation; NAS.
 DR GO; GO:0042127; P:regulation of cell proliferation; NAS.

```

DR      GO; GO:0007367; P:segment polarity determination; NAS.
DR      GO; GO:0008587; P:wing margin morphogenesis; NAS.
DR      InterPro; IPR005817; Wnt.
DR      InterPro; IPR005816; Wnt_grthfactor.
DR      Pfam; PF00110; wnt; 1.
DR      PRINTS; PR01349; WNTPROTEIN.
DR      SMART; SM00097; WNT1; 1.
DR      PROSITE; PS00246; WNT1; 1.
KW      Wnt signaling pathway; Developmental protein; Glycoprotein;
KW      Segmentation polarity protein; Signal.
ET      SIGNAL          1          17
ET      CHAIN           18         468      PROTEIN INT-1.
ET      CARBOHYD        103        103      N-LINKED (GLCNAC. . .) (POTENT
ET      CARBOHYD        108        108      N-LINKED (GLCNAC. . .) (POTENT
ET      CARBOHYD        414        414      N-LINKED (GLCNAC. . .) (POTENT
ET      VARIANT         104        104      C -> S (IN ALLELE WG-IL114).
ET      VARIANT         221        221      G -> D (IN ALLELE WG-IN57).
ET      CONFLICT        182        182      W -> C (IN REF. 2).
ET      CONFLICT        204        204      E -> D (IN REF. 2).
ET      CONFLICT        275        275      N -> T (IN REF. 2).
ET      CONFLICT        297        297      G -> A (IN REF. 2).
ET      CONFLICT        315        315      E -> EE (IN REF. 2).
ET      CONFLICT        364        364      K -> N (IN REF. 2).
ET      CONFLICT        391        391      E -> D (IN REF. 2).
ET      CONFLICT        441        441      E -> D (IN REF. 2).
SQ      SEQUENCE        468 AA;  51986 MW;  AF766972A731E6171 CRC64;

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Query Match 50.2%; Score 1022.5; DB 1; Length 468;
Best Local Similarity 45.7%; Pred. No. 5.8e-82;
Matches 203; Conservative 43; Mismatches 89; Indels 109; Gaps 8;

[illegible]

Db 385 KDLVYLEPSPSFCEKNLRQGILGTHGRQCNETSLGVDGCGLMCCGRGYRRDEVVVVERCA 444

Qy 347 CTFHWCCHVSCRNCTHTRVLHECL 370
 ||||| | | : | :|: ||

De 445 CTFHWCCEVKCKLCRTKKVIYTCL 468

RESULT 8

WN3A_MOUSE

ID WN3A_MOUSE STANDARD; PRT; 352 AA.

AC P27467;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Wnt-3a protein precursor.

GN WNT3A OR WNT-3A.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=91160971; PubMed=2001840;

RA Roelink H., Nusse R.;

RT "Expression of two members of the Wnt family during mouse

RT development -- restricted temporal and spatial patterns in the

RT developing neural tube.";

RL Genes Dev. 5:381-388(1991).

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN

CC TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN

CC CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL

CC TUBE.

CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the

CC extracellular matrix.

CC -!- TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE (DEVELOPING

CC ROOF PLATE), AND MESENCHYME TISSUE SURROUNDING THE UMBILICAL

CC VEINS.

CC -!- SIMILARITY: Belongs to the Wnt family.

CC -----

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CC -----

DR EMBL; X56842; CAA40173.1; -.

DR PIR; A39532; A39532.

DR MGD; MGI:98956; Wnt3a.

DR InterPro; IPR005817; Wnt.

DR InterPro; IPR005816; Wnt_grthfactor.

DR Pfam; PF00110; wnt; 1.

DR PRINTS; PR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1; 1.

DR PROSITE; PS00246; WNT1; 1.

RT mouse embryos and adult brain.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:4519-4523(1990).

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN

CC TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN

CC CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL

CC TUBE.

CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the

CC extracellular matrix.

CC -!- TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE, DORSAL

CC ECTODERM, THE BRANCHIAL ARCHES, AND THE LIMB BUDS.

CC -!- DISEASE: SOME MOUSE MAMMARY TUMORS INDUCED BY MOUSE MAMMARY TUMOR

CC VIRUS (MMTV) CONTAIN A PROVIRUS INTEGRATED INTO A HOST CELL REGION

CC WHICH HAS BEEN NAMED WNT-3.

CC -!- SIMILARITY: Belongs to the Wnt family.

CC -----

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CC -----

DR EMBL; M32502; AAB38109.1; -.

DR FIR; A35503; A35503.

DR MGD; MGI:98955; Wnt3.

DR InterPro; IPR005817; Wnt.

DR InterPro; IPR005816; Wnt_g_rthfactor.

DR Pfam; PF00110; wnt; 1.

DR PRINTS; PR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1; 1.

DR PROSITE; PS00246; WNT1; 1.

KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal;

KW Proto-oncogene; Extracellular matrix.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 355 WNT-3 PROTO-ONCOGENE PROTEIN.

FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 355 AA; 39659 MW; F31CFD65E43E9C17 CRC64;

Query Match 41.4%; Score 843.5; DB 1; Length 355;

Best Local Similarity 46.0%; Pred. No. 2e-66;

Matches 155; Conservative 53; Mismatches 120; Indels 9; Gaps 3;

QY 34 WWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLIRQNPGILHSVSGGLQSAVREC 93

DB 26 WWSLALGQQYTSLAS-----QPLLCSIPGLVPKQLRFCRNYIEIMPSVAEGVKLG IQEC 80

QY 94 KWQFRNRRWNCPTAPGP-HLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCT 152

DB 21 QHQFRGRRWNCTTIDDSLAIFGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICG 140

QY 153 CDYRRRGPGGPDWHWGGCSDNIDFGR LFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFS 212

DB 141 CDSHHKGPPGEGWKWGGCSEDADFGVLVSREFADARENRPDARSAMNKHNNNEAGRTTILD 200

QY 213 EMRQECKCHGMSGSCTVRTCWMRLPTLRAVGDLRDRFDGASRVLYGNRGSNRASRAELL 272

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      | :| | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :
Db    201 HMKLCKCHGLSGSCEVKTCCWQAQPDFRAIGDFLKDKYDSASEMVV---EKHRESRGWVE 257

QY    273 RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCCELLCCGR 332
      | : | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db    258 TLRKYALFKPPTERDLVYYENSPNFCEPNPETGSFGTRDRTCNTVSHGIDGCDLLCCGR 317

QY    333 GHRTTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
      | | | | | : | : | | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db    318 GHNTRTEKRKEKCHCVFHWCCYVSCQECIRIYDVHTC 354

```

RESULT 10

WNT4_XENLA

```

ID    WNT4_XENLA          STANDARD;          PRT;    351 AA.
AC    P49338; Q91927;
DT    01-FEB-1996 (Rel. 33, Created)
DT    01-FEB-1996 (Rel. 33, Last sequence update)
DT    15-SEP-2003 (Rel. 42, Last annotation update)
DE    Wnt-4 protein precursor (XWnt-4).
GN    WNT-4.
OS    Xenopus laevis (African clawed frog).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC    Xenopodinae; Xenopus.
OX    NCBI_TaxID=8355;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=93048810; PubMed=1425335;
RA    McGrew L.L., Otte A.P., Moon R.T.;
RT    "Analysis of Xwnt-4 in embryos of Xenopus laevis: a Wnt family member
RT    expressed in the brain and floor plate.";
RL    Development 115:463-473(1992).
RN    [2]
RP    SEQUENCE OF 261-351 FROM N.A.
RC    TISSUE=Embryo;
RX    MEDLINE=91122437; PubMed=1991549;
RA    Christian J.L., Gavin B.J., McMahon A.P., Moon R.T.;
RT    "Isolation of cDNAs partially encoding four Xenopus
RT    Wnt-1/int-1-related proteins and characterization of their transient
RT    expression during embryonic development.";
RL    Dev. Biol. 143:230-234(1991).
CC    -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC    TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC    SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE
CC    REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
CC    DIAMETERS.
CC    -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC    extracellular matrix.
CC    -!- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN AND FLOOR PLATE.
CC    -!- DEVELOPMENTAL STAGE: EXPRESSION DURING THE NEURULA THROUGH TADPOLE
CC    STAGES OF DEVELOPMENT.
CC    -!- SIMILARITY: Belongs to the Wnt family.
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RESULT 11

WNT3_HUMAN

ID WNT3_HUMAN STANDARD; PRT; 355 AA.

AC P56703; Q9H1J9;

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Wnt-3 proto-oncogene protein precursor.

GN WNT3 OR INT4.

OS Homo sapiens (Human).

QC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Testa T.T., Mossakowska D.E., Carter P.S., Hu E., Zhu Y.,

RA Kelsell D.P., Murdock P.R., Herrity N.C., Lewis C.J., Cross D.A.,

RA Culbert A.A., Reith A.D., Barnes M.R.;

RT "Molecular cloning and characterization of six novel human WNT genes.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

EX MEDLINE=21490205; PubMed=11604997;

RA Katoh M.;

RT "Molecular cloning and characterization of human WNT3.";

RL Int. J. Oncol. 19:977-982(2001).

RN [3]

RP SEQUENCE OF 1-333 FROM N.A.

EX MEDLINE=94063935; PubMed=8244403;

RA Roelink H., Wang J., Black D.M., Solomon E., Nusse R.;

RT "Molecular cloning and chromosomal localization to 17q21 of the human WNT3 gene.";

RL Genomics 17:790-792(1993).

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN

CC TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN

CC CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL

CC TUBE (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the

CC extracellular matrix.

CC -!- SIMILARITY: Belongs to the Wnt family.

CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AY009397; AAG38657.1; -.

DR EMBL; AB067628; BAB70502.1; -.

DR PIR; A47536; A47536.

DR Genew; HGNC:12782; WNT3.

DR MIM; 165330; -.

DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Testa T.T., Mossakowska D.E., Carter P.S., Hu E., Zhu Y.,
 RA Kelsell D.P., Murdock P.R., Herrity N.C., Lewis C.J., Cross D.A.,
 RA Culbert A.A., Reith A.D., Barnes M.R.;
 RT "Molecular cloning and characterization of six novel human WNT
 RT genes.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21205589; PubMed=11283799;
 RA Jordan B.K., Mohammed M., Ching S.T., Delot E., Chen X.N., Dewing P.,
 RA Swain A., Rao P.N., Elejalde B.R., Vitain E.;
 RT "Up-regulation of wnt-4 signaling and dosage-sensitive sex reversal in
 RT humans.";
 RL Am. J. Hum. Genet. 68:1102-1109(2001).
 RN [3]
 RP SEQUENCE OF 27-351 FROM N.A.
 RA Pearce A.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 210-329 FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=94221588; PubMed=8168088;
 RA Huguet E.L., McMahon J.A., McMahon A.P., Bicknell R., Harris A.L.;
 RT "Differential expression of human Wnt genes 2, 3, 4, and 7B in human
 RT breast cell lines and normal and disease states of human breast
 RT tissue.";
 RL Cancer Res. 54:2615-2621(1994).
 RN [5]
 RP SEQUENCE OF 1-26 FROM N.A.
 RA Peltoketo H., Heikkila M., Vainio S.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE OF 1-26 FROM N.A.
 RA Sim U.E., Smith A., Szilagi E., Ioannou P., Lindsay M.H., Little M.H.;
 RT "Expression of Wnt-4 can be regulated by the Wilms' tumor suppressor
 RT gene, WT1.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
 CC SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE
 CC REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
 CC DIAMETERS (BY SIMILARITY). OVEREXPRESSION MAY BE ASSOCIATED WITH
 CC ABNORMAL PROLIFERATION IN HUMAN BREAST TISSUE.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix.
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC -----
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CC -----

DR EMBL; AY009398; AAG38658.1; -.

DR EMBL; AF316543; AAK51699.1; -.

DR EMBL; AL031281; CAB52601.1; -.

DR EMBL; AF335591; AAK25765.1; -.

DR EMBL; AY033057; AAK50427.1; -.

DR Genew; HGNC:12783; WNT4.

DR MIM; 603490; -.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.

DR GO; GO:0007267; P:cell-cell signaling; NAS.

DR GO; GO:0007275; P:development; NAS.

DR InterPro; IPR005817; Wnt.

DR InterPro; IPR005816; Wnt_grthfactor.

DR Pfam; PF00110; wnt; 1.

DR PRINTS; FR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1; 1.

DR PROSITE; PS00246; WNT1; 1.

KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 351 WNT-4 PROTEIN.

FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 106 106 T -> I (IN REF. 1).

FT CONFLICT 111 111 F -> L (IN REF. 1).

SEQUENCE 351 AA; 39051 MW; 465D08755C992DA8 CRC64;

Query Match 41.3%; Score 840; DB 1; Length 351;

Best Local Similarity 44.8%; Pred. No. 3.9e-66;

Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

Qy 14 TLLLAIAALPAALAANSSGRWVGIVNVASSTNLITDSKSLQLVLEPSLQLLSRKQRRLLIP 73

Db 9 SLRLLLVFAVFSAASN-----WLYLAKLSSVGSISEEETCE-----KLKGLIQRQVQMCK 58

Qy 74 QNPGILHSVSGGLQSAVRECKWQFRNRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133

Db 59 RNLEVMDSVRRGAQLAIEECQYQFRNRWNCSTLDSLPLVFGKVVTQGTREAAFYVAISS 118

Qy 134 GVTHSVARSCSEGSIESCTCYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGR- 192

Db 119 GVFAVTRACSSGELEKCGCDRTVHGVSPQGFQWGCSDNIAYGVAFSQSFVDVRERSKG 178

Qy 193 --DLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDLRDRF 250

Db 172 ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKF 238

Qy 251 DGASRVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310

Db 239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLESPDFCEQDMRSGVLGT 291

Qy 311 AGRACNSSSPALDGCELLCCGRGHRTRTQRTVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369

Db 292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCCKFWCCFVKCRQCQRLVELHTC 350

WNT4_MOUSE

ID WNT4_MOUSE STANDARD; PRT; 351 AA.
AC P22724;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Wnt-4 protein precursor.
GN WNT4 OR WNT-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91122634; PubMed=2279700;
RA Gavin B.J., McMahon J.A., McMahon A.P.;
RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal
RT and adult mouse development.";
RL Genes Dev. 4:2319-2332(1990).
CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING
CC MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO
CC SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY). SEEMS TO BE
CC INVOLVED IN KIDNEY DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- TISSUE SPECIFICITY: IN ADULTS IN LUNG AND BRAIN.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M89797; AAA40566.1; -.
DR PIR; C36470; C36470.
DR MGD; MGI:98957; Wnt4.
DR GO; GO:0042445; P:hormone metabolism; IMP.
DR GO; GO:0007292; P:oogenesis; IMP.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0007548; P:sex differentiation; IMP.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 351 WNT-4 PROTEIN.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 351 AA; 39049 MW; 7E1C5C739BE939D9 CRC64;

Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 8.7e-66;
 Matches 160; Conservative 55; Mismatches 124; Indels 20; Gaps 4;

```

Qv      14 TLLALAAALPAALAAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRIR 73
      :| | : | : | | :| | : | | :| | :| | :| | :| | :| | :| |
Db      9 SLRLLVFAVFSAAASN-----WLYLAKLSSVGSISEEETCE-----KLKGLIQRQVQMCK 58

Qy      74 QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      59 RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFFVYAIS 118

Qy     134 GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGCSNIDFGRLFGREFVDSGEKGR- 192
      || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     119 GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSNIAYGVAFSQSFDVRRERSKG 178

Qy     193 --DLRFLMNLHNEAGRITTVFSEMRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDLRDRF 250
      | | | | | | | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     179 ASSSRALMNLHNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVPPFRQVGHALKEKF 238

Qy     251 DGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDIRSGVLGT 291

Qy     311 AGRACNSSSPALDGCCELLCCGRGHRTTRTQVTERCNC'TFHWCCHVSCRNCTHTRVLHEC 369
      || | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     292 RGRTCNKTSKALDGCCELLCCGRGFHTAQVELAERCGCRFHWCCEVVKCRQCQRLVEMHTC 350
  
```

RESULT 14

WNT4_RAT

ID WNT4_RAT STANDARD; PRT; 351 AA.

AC Q9QXQ5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Wnt-4 protein precursor.

GN WNT4 OR WNT-4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Corpus luteum;

RA Lacher M.D., Walther P.R., Lareu R., Dharmarajan A.M., Friis R.R.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN

CC TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING

CC MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO

CC SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the

CC extracellular matrix.

CC -!- SIMILARITY: Belongs to the Wnt family.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

GN WNT4 OR WNT-4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=95032034; PubMed=7945308;
 RA Yoshioka H., Ohuchi H., Nohno T., Fujiwara A., Tanda N.,
 RA Kawakami Y., Noji S.;
 RT "Regional expression of the Cwnt-4 gene in developing chick central
 RT nervous system in relationship to the diencephalic neuromere D2 and a
 RT dorsal domain of the spinal cord.";
 RL Biochem. Biophys. Res. Commun. 203:1581-1588(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96063018; PubMed=7579581;
 RA Tanda N., Kawakami Y., Saito T., Noji S., Nohno T.;
 RT "Cloning and characterization of Wnt-4 and Wnt-11 cDNAs from chick
 RT embryo.";
 RL DNA Seq. 5:277-281(1995).
 CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
 CC TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING
 CC MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN INTO THE
 CC NEUROMERE D2 AND IN DIFFERENTIATION OF THE DORSAL REGION OF THE
 CC SPINAL CORD. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE DIENCEPHALON
 CC NEUROMERE D2.
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC -----
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 CC -----
 DR EMBL; D31900; BAA06698.1; ..
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 351 WNT-4 PROTEIN.
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 351 AA; 38963 MW; D22DC689284A961C CRC64;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 10:44:42 ; Search time 20 Seconds
(without alignments)
1779.121 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2036
Sequence: 1 MGLWALLPGWVSATLLLLALA.....WCCHVSCRNCTHTRVLHECL 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%									
Result		Query									
No.	Score	Match	Length	DB	ID	Description					
1	2036	100.0	370	1	TVHUT1	transforming prote					
2	2021	99.3	370	1	TVMST1	transforming prote					
3	2021	99.3	370	1	TVMVT1	transforming prote					
4	1671	82.1	369	2	S13721	Wnt-1 protein prec					
5	1595	78.3	370	2	S15013	wnt-1 protein - ze					
6	1463	71.9	371	1	TVXLT1	transforming prote					
7	1022.5	50.2	468	2	A29650	wingless (wg) prot					
8	998	49.0	469	1	TVFFT1	transforming prote					
9	873.5	42.9	352	2	A49146	developmental regu					
10	866.5	42.6	303	2	S41156	wingless protein -					
11	843.5	41.4	352	2	A39532	Wnt-3A protein - m					
12	843.5	41.4	355	2	A35503	Wnt-3 protein - mo					
13	836	41.1	351	2	C36470	Wnt-4 protein - mo					

14	827	40.6	351	2	JC2451	Cwnt-4 protein pre
15	822.5	40.4	352	2	A48828	wingless homolog X
16	787.5	38.7	365	2	JC7694	soluble-type glyco
17	785	38.6	360	2	S00834	int-1-like protein
18	781	38.4	360	2	B36470	Wnt-2 protein - mo
19	780.5	38.3	364	2	F36470	Wnt-6 protein - mo
20	769	37.8	379	2	D36470	Wnt-5a protein - m
21	766.5	37.6	365	2	A48914	proto-oncogene Wnt
22	766.5	37.6	372	2	T09612	secreted glycoprot
23	759.5	37.3	333	2	A47536	gene WNT3 protein
24	753	37.0	359	2	A56549	cell-cell signalin
25	749	36.8	372	2	E36470	Wnt-5b protein - m
26	742	36.4	417	2	B59392	Wnt10a protein pro
27	741	36.4	417	2	JC7693	soluble-type glyco
28	728.5	35.8	357	2	B56549	cell-cell signalin
29	724.5	35.6	360	2	S34173	wnt-5c protein - A
30	722.5	35.5	442	2	I50110	Wnt10a protein - z
31	716.5	35.2	349	2	H36470	Wnt-7b protein - m
32	711.5	34.9	349	2	G36470	Wnt-7a protein - m
33	707	34.7	389	2	I49263	potential oncogene
34	707	34.7	389	2	A59392	Wnt10b protein pre
35	703	34.5	360	2	T26037	hypothetical prote
36	694	34.1	360	2	S32695	Wnt-2 protein - Ca
37	690	33.9	134	2	I50729	gene Wnt-1 protein
38	684	33.6	352	2	S24559	Wnt-2 protein - fr
39	678	33.3	348	2	T10502	Wnt-7a protein - I
40	671	33.0	1004	2	A48821	Wnt-5 protein - fr
41	660.5	32.4	354	2	S34378	wnt-11 protein - m
42	641	31.5	353	2	I51572	maternal protein -
43	631	31.0	372	2	S32694	Wnt-1 protein - Ca
44	630.5	31.0	354	2	JC4152	Wnt-11 protein pre
45	630.5	31.0	358	2	I50506	gene. wnt8b protein

ALIGNMENTS

RESULT 1

TVHUT1

transforming protein int-1 - human

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999

C;Accession: A24674

R;van Ooyen, A.; Kwee, V.; Nusse, R.

EMBO J. 4, 2905-2909, 1985

A;Title: The nucleotide sequence of the human int-1 mammary oncogene; evolutionary conservation of coding and non-coding sequences.

A;Reference number: A24674; MUID:86055728; PMID:2998762

A;Accession: A24674

A;Molecule type: DNA

A;Residues: 1-370 <VAN>

A;Cross-references: GB:X03072; NID:g33935; PIDN:CAA26874.1; PID:g33936

C;Genetics:

A;Gene: GDB:WNT1; INT1

A;Cross-references: GDB:120101; OMIM:164820

A;Map position: 12q13-12q13

A;Introns: 35/2; 120/1; 208/3

C;Superfamily: int-1 transforming protein

C;Keywords: proto-oncogene; transforming protein; transmembrane protein

F;1-48/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 2036; DB 1; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.1e-160;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60
      |||
Db       1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60

QY     61 LQLLSRKQRRRLIRQNP GILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
      |||
Db     61 LQLLSRKQRRRLIRQNP GILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120

QY    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180
      |||
Db    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180

QY    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240
      |||
Db    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240

QY    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCT 300
      |||
Db    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCT 300

QY    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTTRTQVTERCNCCTFHWCCHVSCRNC 360
      |||
Db    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTTRTQVTERCNCCTFHWCCHVSCRNC 360

QY    361 THTRVLHECL 370
      |||
Db    361 THTRVLHECL 370
```

RESULT 2

EVMS1

transforming protein int-1 - mouse

N;Alternate names: Wnt-1 protein

C;Species: Mus musculus (house mouse)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Jun-1999

C;Accession: A23447; A36470; A01358

R;Fung, Y.K.T.; Shackleford, G.M.; Brown, A.M.C.; Sanders, G.S.; Varmus, H.E.
Mol. Cell. Biol. 5, 3337-3344, 1985

A;Title: Nucleotide sequence and expression in vitro of cDNA derived from mRNA
of int-1, a provirally activated mouse mammary oncogene.

A;Reference number: A93068; MUID:86310810; PMID:3018519

A;Accession: A23447

A;Molecule type: mRNA

A;Residues: 1-370 <FUN>

A;Cross-references: GB:M11943; NID:g198423; PIDN:AAA39322.1; PID:g293671

A;Note: the authors translated the codon GTG for residue 242 as Gly and GGC for
codon 243 as Val

R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.

Genes Dev. 4, 2319-2332, 1990

A;Title: Nucleotide sequence of a cDNA encoding Wnt-1 of the Mexican axolotl *Ambystoma mexicanum*.
A;Reference number: S13721; MUID:91081334; PMID:2259633
A;Accession: S13721
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-369 <BUS>
A;Cross-references: EMBL:X55270; NID:g62424; PIDN:CAA38991.1; PID:g62425
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1990
R;Busse, U.; Guay, J.; Seguin, C.
Nucleic Acids Res. 19, 981, 1991
A;Title: Nucleotide sequence of a cDNA encoding Wnt-1 of the Mexican axolotl *Ambystoma mexicanum*.
A;Reference number: S13722; MUID:91204483; PMID:2017393
A;Contents: annotation; reprinted sequence figure
C;Genetics:
A;Gene: Wnt-1
C;Superfamily: int-1 transforming protein

Query Match 82.1%; Score 1671; DB 2; Length 369;
Best Local Similarity 81.7%; Pred. No. 2.7e-130;
Matches 290; Conservative 37; Mismatches 28; Indels 0; Gaps 0;

```

QY      26 LLALAALPAALAAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLIRQN 75
      :|| :|| || :||||||:|||| :||||||:|:|:||||:|||||||:|||||
DB      25 ILAFSSLSNTLAVNNSGRWWGVVNVVTSTNLLTDTKNVQLVLDPSLQLLSRKQRRLLIRQN 74

QY      76 PGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITSAGV 135
      |||||:| :|||:|:|||||:||||| | :|:|||||:|||||||:|||||
DB      75 PGILHSINSGLQSAMKECKWQFRSRRWNCPTTGGDNIFGKIVNKGCRETAFIFAITSAGV 134

QY     136 THSVARSCSEGSIESCTCDYRRRGPGGPDWHWGCSDNIDFGRLFGREFVDSGEKGRDLR 195
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB     135 THSVARSCSEGSIESCTCDYRRRGPGGTDWHWGCSDNIDFGRVFGREFVDSSERGRDLR 194

QY     196 FLMNLHNEAGRRTTVFSEMRQECKCHGMSGSCVTRTCWMRLPTLRAVGDVLRDRFDGASR 255
      :||| ||||| |||||:||||| ||||| ||||| ||||| :|:|||||
DB     195 YLMNRHNEAGRMTVFSEMKQECKCHGMSGSCAVRTCWMRLPTFRAVGDFLKDRFDGASR 254

QY     256 VLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRAC 315
      |:|:|:||||| : ||||| ||||| ||||| |||||:|: ||:|:|
DB     255 VIYGNKGSNRASRVQTHHLEPENPTHKPPSPQDLVYFEKSPNFCTYNGKTGTSGTSGRV 314

QY     316 NSSSPALDGCCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRNCTHTRVLHECL 370
      |||| | |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB     315 NSSSLGLDGCCELLCCGRGYRTKTQVTERCHCTFHWCCHVSCNCTNTQVLHECL 369

```

RESULT 5

S15013

wnt-1 protein - zebra fish

C;Species: *Brachydanio rerio* (zebra fish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C;Accession: S15013

R;Molven, A.; Njolstad, P.R.; Fjose, A.

EMBO J. 10, 799-807, 1991

A;Title: Genomic structure and restricted neural expression of the zebrafish wnt-1 (int-1) gene.
A;Reference number: S15013; MUID:91184125; PMID:2009859
A;Accession: S15013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <MOL>
A;Cross-references: GB:X58880; GB:X57301; NID:g62556; PIDN:CAA41687.1; PID:g833600
C;Genetics:
A;Gene: wnt-1
C;Superfamily: int-1 transforming protein

Query Match 78.3%; Score 1595; DB 2; Length 370;
Best Local Similarity 75.7%; Pred. No. 5.1e-124;
Matches 281; Conservative 47; Mismatches 41; Indels 2; Gaps 2;

```

Qy      1 MGLWALLPGWVSATLLALLAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60
      | : |||  | | :| ::|  | :||| ||||| ||||| :||| :||
Db      1 MRVLALLLA-VKAACVLLVSSLTGTGAVNNSGRWWGIVNVASSGNLLTNSKNVQLVIDPS 59

Qy     61 LQLLSRKQRRIRQNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
      | ||||:|:| ||||| |||:| :||| ||||| ||||| |::| |||||
Db     60 LALLSRRQRKLIRQNPGILHAIAAGLHTAIKECKWQFRNRRWNCPTTHSPNVFGKIVNRG 119

Qy    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLP 180
      |||||:| ||||| |||:| ||||| ||||| ||||| ||||| ||||| :||| :|
Db    120 CRETAFVFAITSAGVTHAVARSCSECAIESCTCDYRRRGPGGPDWHWGGCSDNVEFGRMF 179

Qy    181 GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSGCTVRTCWMRLPTLR 240
      ||||| | :||| :| ||||| || |||:| ||||| ||||| ||||| ||||| :|
Db    180 GREFVDSSERGRDLRYLTNLHNNEAGRMTVASEMQECKCHGMSGSGCTVRTCWMRLPSFR 239

Qy    241 AVGDVLRDRFDGASRVLYGNRGSNRAS-RAELLRLEPEDPAHKPPSPHDLVYFEKSPNFC 299
      ||| | :||| ||||| :| :||| ||| :| ||||| :||| || ||||| |||||
Db    240 LVGDYLRDRFDGASRVVYANKGSNRASHRADPRHLEPENPAHKLPSSRDLVYFEKSPNFC 299

Qy    300 TYSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRN 359
      :|:| :| |||:| ||||| ||||| ||||| ||||| :||| :||| ||||| |||||
Db    300 SYNGKTGTHGTSGRTCNSSSPALDGCELLCCGRGYKTRMEQVTERCHCTFHWCCHVSCLN 359

Qy    360 CTHTRVLHECL 370
      || | :|:|
Db    360 CTSTQTVHQCL 370

```

RESULT 6
TVXLT1
transforming protein int-1 precursor - African clawed frog
N;Alternate names: pxwnt-1 protein
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C;Accession: S02113; S41630
R;Noordermeer, J.; Meijlink, F.; Verrijzer, P.; Rijsewijk, F.; Destree, O.
Nucleic Acids Res. 17, 11-18, 1989
A;Title: Isolation of the Xenopus homolog of int-1/wingless and expression during neurula stages of early development.

A29650

wingless (wg) protein precursor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: int-1 homolog (Dint-1)

C;Species: *Drosophila melanogaster*

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999

C;Accession: A29650; S41671; S41157

R;Rijsewijk, F.; Schuermann, M.; Wagenaar, E.; Parren, P.; Weigel, D.; Nusse, R.
Cell 50, 649-657, 1987

A;Title: The *Drosophila* homolog of the mouse mammary oncogene int-1 is identical to the segment polarity gene wingless.

A;Reference number: A29650; MUID:87273528; PMID:3111720

A;Accession: A29650

A;Molecule type: mRNA

A;Residues: 1-468 <RIJ>

A;Cross-references: GB:M17230; NID:g157765; PIDN:AAA28647.1; PID:g157766

R;van den Heuvel, M.; Harryman-Samos, C.; Klingensmith, J.; Perrimon, N.; Nusse, R.

EMBO J. 12, 5293-5302, 1993

A;Title: Mutations in the segment polarity genes wingless and porcupine impair secretion of the wingless protein.

A;Reference number: S41671; MUID:94085405; PMID:8262072

A;Accession: S41671

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-468 <VAN>

R;Nagy, L.M.; Carroll, S.

Nature 367, 460-463, 1994

A;Title: Conservation of wingless patterning functions in the short-germ embryos of *Tribolium castaneum*.

A;Reference number: S41156; MUID:94150623; PMID:8107804

A;Accession: S41157

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 101-468 <NAG>

C;Genetics:

A;Gene: FlyBase:wg

A;Cross-references: FlyBase:FBgn0004009

C;Superfamily: int-1 transforming protein

C;Keywords: glycoprotein

Query Match 50.2%; Score 1022.5; DB 2; Length 468;

Best Local Similarity 45.7%; Pred. No. 1.2e-76;

Matches 203; Conservative 43; Mismatches 89; Indels 109; Gaps 8;

Qy 31 SGR-----WWGIVNVASSTNLLTDSKSLQLVLEPSL-QLLSRKQRRLLIRQNPGILHSVSG 84
||| ||| | : : : : : | ||||| : | ||| : :

Db 30 SGRGRGSMWWGIAKVGEPPNI-----TPIMYMDPAIHSTLRRKQRRLLVRDNPGLGALVK 84

Qy 85 GLQSAVRECKWQFRNRRWNCPT---APGPHLFGKIVNRGCRETAFIFAITSAGVTHSVAR 141
| | : || : ||||| | : | : ||||| : ||||| : || : ||| : ||| :

Db 85 GANLAISECQHQFRNRRWNCSTRNFSRGKNLFGKIVDRGCRETSFIYAITSAVTHSIAR 144

Qy 142 SCSEGSIESCTCDY--RRRG-----GGPDWHWGGCSDNIDFGRLFGREFVDSGE 189
: |||| : ||||| : | | | | | ||||| || | |||| : || :

Db 145 ACSEGTIESCTCDYSHQSRSPQANHQAQSVAGVRDWEWGGCSDNIGFGFKFSREFVDTGE 204

Qy 190 KGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDVLRDR 249

Qy	165	WHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMS	224
		: : : : :	
Db	180	WECGGCSDNIGFGFKFSREFVDGTGDRGNLREKMNLHNNNEAGRAHVQAEMRQECKCHGMS	239
Qy	225	GSCTVRTCWMLPTLRAVGDVLRDRFDGASRV-----	256
		: : : :	
Db	240	GSCTVKTCWMRLANFRVIGDNLKARFDGATRVQVTTS LRATNALAPVSPNAAGSNSVSGSN	299
Qy	257	-----LY-----GNRGSNRA	266
		:	
Db	300	GLIIPQSGLVYGEERMLNDHMPDILLENSHPISKIHHPNMPSNLSLPQAGQRGGRNG	359
Qy	267	SRAEL-----LRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGACNSSSP	320
		: : : : : :	
Db	360	RROGRNHNRHYHFQLNPHNPEHKPPGSKDLVYLDPSPSFCEKNLRQGILGTHGRQCNETSL	419
Qy	321	ALDGCELLCCGRGHRTRTQRVTERCNCTFWHCCHVSCRCNTHTRVLHECL	370.
		: : : : : : : :	
Db	420	GVDGCGLMCCGRGYRRDEVVVVDRCACFTFWCCCEVKCKLCRTKKVIYTCL	469

A49146

C: Species: *Xenopus laevis* (African clawed frog)

Q: Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995.

McGrew, L.L.; Otte, A.P.; Moon, R.T.

A, Title: Analysis of Xwnt-4 in embryos of *Xenopus laevis*: a Wnt family member expressed in the brain and floor plate.

A: Accession: A49146

A; Molecule type: mRNA

A; Experimental source: neurula stage embryos

R: Christian, J.L.; Gavin, B.J.; McMahon, A.P.; Moon, R.T.

A;Title: Isolation of cDNAs partially encoding four *Xenopus* Wnt-1/int-1-related proteins and characterization of their transient expression during embryonic development.

A, Accession: C49764

A; Molecule type: mRNA

A;Cross-references: GB:M55055

Query Match 42.9%; Score 873.5; DB 2; Length 352;

Matches 164; Conservative 62; Mismatches 121; Indels 21; Gaps 5;

QY 6 L L P G W S A T L L L A L A A L P A A L A A N S S G R W W G I V N V A S S T N L L T D S K S L Q L V L E P S L Q L L S 65
: | : : | : : | : : | : | : : | : : : : : : |

Db 1 MTPEYFLRSLMMILAVFSANASN-----WLYLAKLSSVGSISEEETCEKLKGP-----I 50

Qy 66 RKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTA-PGPHLFGKIVNRGCRET 124
 ::| :: ::| ::| | | | :| ::| | | | | | | | | | :| | | | | | |

Db 51 QRQVQMCKRNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDTGNQVFGKIINRGTTREA 110

Qy 125 AFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREF 184
 ||::| | | | | | | | | | | | :| | | | | | | | | | :| | | | |

Db 111 AFVYAITSAAGVTHSVTRACSSGDLEKCGCDRTVHGVSPQGFQWSGCSDNILYGVAFSQSF 170

Qy 185 VDSGEK---GRDLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGCTVTRTCWMRLPTLRA 241
 || | : | | | | | | | | | | : : || | | | | : | | | | | | | | | |

Db 171 VDVRERSKGGSSSRALMNLHNNEAGRKAILNNMRVECKCHGVSGSCEVKTCKWKAMPTFRK 230

Qy 242 VGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTY 301
 ||:| | ::| | | | : | | | : | | | : | | | : | | | : | | | : |

Db 231 VGNVLKEKFDGATEVEQKIGSTKV-----LVPKNSQFKPHTDEDLVYLDSSPDCFCDH 283

Qy 302 SGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRTVTERCNCTFHWCCCHVSCRNCT 361
 : | | | | | | | : | | : | | | | : | | | | | | | | | | | | | | |

Db 284 DLKNGVLGTTGRDCNKTSKAIDGCELMCCGRGFHTEEEVEIVERCSCKFHWCCFVKCKQCH 343

Qy 362 HTRVLHEC 369
 : | |

Db 344 KVVMHTC 351

RESULT 10

S41156

wingless protein - red flour beetle (fragment)

C;Species: Tribolium castaneum (red flour beetle)

C;Date: 07-Sep-1994 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997

C;Accession: S41156

R;Nagy, L.M.; Carroll, S.

Nature 367, 460-463, 1994

A;Title: Conservation of wingless patterning functions in the short-germ embryos of Tribolium castaneum.

A;Reference number: S41156; MUID:94150623; PMID:8107804

A;Accession: S41156

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-303 <NAG>

C;Genetics:

A;Gene: wg

C;Superfamily: int-1 transforming protein

C;Keywords: glycoprotein

Query Match 42.6%; Score 866.5; DB 2; Length 303;

Best Local Similarity 53.5%; Pred. No. 5.4e-64;

Matches 162; Conservative 39; Mismatches 61; Indels 41; Gaps 6;

Qy 109 GPHLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCD--YRRR----GPGG 162
 | :| | | | | ::| | | | | :| | | | | | | | | | | | :| :| | | | |

Db 1 GKNLFGKIVDKGCRETAFIYAITSAAVTHAIARACSEGSIDTCNCETHYKGRPHVSGNGG 60

Qy 163 -----PDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRRTTVFSEMRQ 216
 | :| | | | | | | | | | | | | | | | :| | | | | | | | | |

Qy 255 RVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRA 314
 Db 240 EMVV---EKHRESRGWVETLRPRYTYFKVPTERDLVYYEASPNFCEPNPETGSFGTRDRT 296

Qy 315 CNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
 Db 297 CNVSSHGIDGCDLLCCGRGHNARTERRREKCHCVFHWCCYVSCQECTRVYDVHTC 351

RESULT 12

A35503

Wnt-3 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Jul-1999

C;Accession: A35503

R;Roelink, H.; Wagenaar, E.; Lopes da Silva, S.; Nusse, R.

Proc. Natl. Acad. Sci. U.S.A. 87, 4519-4523, 1990

A;Title: Wnt-3, a gene activated by proviral insertion in mouse mammary tumors, is homologous to int-1/Wnt-1 and is normally expressed in mouse embryos and adult brain.

A;Reference number: A35503; MUID:90280407; PMID:2162045

A;Accession: A35503

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-355 <ROE>

A;Cross-references: GB:M32502; NID:g198428; PIDN:AAB38109.1; PID:g293672

C;Superfamily: int-1 transforming protein

Query Match 41.4%; Score 843.5; DB 2; Length 355;
 Best Local Similarity 46.0%; Pred. No. 5.1e-62;
 Matches 155; Conservative 53; Mismatches 120; Indels 9; Gaps 3;

Qy 34 WWGIVNVASSTNLLTDEKSLQLVLEPSLQLLSEKQRLIRQNPGLHVSVCGLQSAVREC 93
 Db 26 WWSLAI.GQQYTSLAS-----QPLLCGSIPGLVPKQLRFCRNYIEIMPSVAEGVKLGIOEC 30

Qy 94 KWQFRNRRWNCPTAPGP-HLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCT 152
 Db 81 QHQFRGRRWNCTTIDDSLAIFGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICG 140

Qy 153 CDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNNEAGRTTVFS 212
 Db 141 CDSHHKGPPGEGWKWGGCSEDADFGVLVSREFADARENRPDARSAMNKHNEAGRTTILD 200

Qy 213 EMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLRDRFDGASRVLYGNRGSNRASRAELL 272
 Db 201 HMHLKCKCHGLSGSCEVKTCWWAQPDFRAIGDFLKDKYDSASEMVV---EKHRESRGWVE 257

Qy 273 RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCELLCCGR 332
 Db 258 TLRAKYALFKPPTERDLVYYENSPNFCEPNPETGSFGTRDRTCNVTSHGIDGCDLLCCGR 317

Qy 332 GHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
 Db 318 GHNTRTEKRKEKCHCVFHWCCYVSCQECIRIYDVHTC 354

C36470

C;Species: Mus musculus (house mouse)

C;Accession: C36470

Genes Dev. 4, 2319-2332, 1990

A;Reference number: A36470; MUID:91122634; PMID:2279700

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-351 <GAV>

A;Cross-references: GB:M89797; NID:g202401; PIDN:AAA40566.1; PID:g202402

C; Superfamily: int-1 transforming protein

Query Match 41.1%; Score 836; DB 2; Length 351;
Best Local Similarity 44.5%; Pred. No. 2.1e-61;
Matches 160; Conservative 55; Mismatches 124; Indels 20; Gaps 4;

Qy	14	TLLLALAAALPAALAAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLR	73
Db	9	SLRLLLVFAVFSAAASN-----WLYLAKLSSVGSISEEETCE-----KLKGLIQRQVQMCK	58
Qy	74	QNPGLHHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS	133
Db	59	RNLEVMDSVRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVQTGTREAAFVYAISS	118
Qy	134	GVTHSVARSCSEGSIESCTCYRRRGPGGPDWHWGGCSDNIDFGRLFGRFVDSGEKGR-	192
Db	119	GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFDVWRERSKG	178
Qy	193	--DIRFLMNLHNNAGRTTVFSEMRQECKCHGMSGSCTVRTCWMRLPTLRAVGDLRDRF	250
Db	179	ASSSRALMNLHNNAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKF	238
Qy	251	DGASRVLYGNRGSNRASRAELRLLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT	310
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDIRSGVLGT	291
Qy	311	AGRACNSSSPALDGCCELLCCGRGHRTFTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC	369
Db	292	RGRTCNKTSKAILDGCCELLCCGRGFHTAQVELAERCGRFHWCCFVKRCQCRQLVEMHTC	350

JC2451

C; Species: Gallus gallus (chicken)

C:Accession: JC2451

R;Yoshioka, H.; Ohuchi, H.; Nohno, T.; Fujiwara, A.; Tanda, N.; Kawakami, Y.; Noji, S.

Biochem. Biophys. Res. Commun. 203, 1581-1588, 1994

A; Title: Overlapping expression of Xwnt-3A and Xwnt-1 in neural tissue of *Xenopus laevis* embryos.

A;Accession: A48828

A;Molecule type: mRNA

A;Note: sequence extracted from NCBI backbone (NCBIP:121343)

C;Superfamily: int-1 transforming protein

Query Match 40.4%; Score 822.5; DB 2; Length 352;
Best Local Similarity 43.4%; Pred. No. 2.7e-60;
Matches 154; Conservative 57; Mismatches 133; Indels 11; Gaps 4;

Qy	16	LLALAALPAALAAANSSGRWGVINVASSTNLLTDSKSLQVLVLEPSLQLLSRKQRRRIQRN	75
Db	7	LLLIIGLHQVLATYPI--WWSLAVGQQYSSLGT----QPIPCGTIPGLVAKQMRFCRNY	59
Qy	76	PGILHSVSGGLQSAVRECKWQFRNRRWNCPTA-PGPHLFGKIVNRGCRETAFIFAITSAG	134
Db	60	MEIMPSVAEGVKIGIQECQHQFRGRRWNCTTVNDNLAIFGPVLDKATRESAFVHAIASAG	119
Qy	135	VTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKCRDL	194
Db	120	VAFVATRSCEGSATTCGCDTHHKGPFGEGWKWGGCSEDMDFGSMVSREFADARENRPDA	179
Qy	195	RFLMNLHNNEAGRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLRDRFDGAS	254
Db	180	RSAMNRHNNEAGRTSILDHRHLKCKCHGLSGSCEVKTCWWSQPDFRVIGDYLKDKYDSAS	239
Qy	255	RVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCTYSGRLGTTAGTAGRA	314
Db	240	EMVV--EKHRESRGWVETLRPKYTFFKPPIERDLIYYESSPNFCEPNPETGSFGTRDRE	296
Qy	315	CNSSSPALDGCELLCCGRGHRTRTQVTERCNCTFHWCCHVSCRNCTHTRVLHEC	369
Db	297	CNVTSHGIDGCDLLCCGRGQNRTEKRKEKCHCIFHWCCYVSCQECMRVYDVHTC	351

Job time : 21 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: January 21, 2004, 10:37:11 ; Search time 44 Seconds ..
(without alignments)
1334.746 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2036
Sequence: 1 MGLWALLPGWVSATLLLLALA.....WCCHVSCRNCTHTRVLHECL 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	
1	2036	100.0	370	20	AAV56108	Human int-1 mammar
2	2036	100.0	370	21	AAV70733	Human Wnt-1 protei
3	2036	100.0	370	21	AAV57594	Human Wnt-1 protei
4	2036	100.0	370	24	AAE34038	WNT-1 protein. Un
5	2036	100.0	370	24	ABU55882	Human WNT-1. prote
6	2025	99.5	370	21	AAB19786	Human Wnt-1 protei
7	1022.5	50.2	468	22	ABB61007	Drosophila melanog
8	843.5	41.4	352	21	AAV57596	Murine Wnt-3a prot
9	840.5	41.3	355	20	AAW30618	Human Wnt-3 protei
10	840	41.3	351	20	AAV41719	Human PRO864 prote
11	840	41.3	351	21	AAB44275	Human PRO864 (UNQ4
12	840	41.3	351	21	AAV57270	Wnt-4AF and Wnt-5c
13	840	41.3	351	21	AAV57273	Wnt-4AF and Wnt-5c
14	840	41.3	351	22	AAU29063	Human PRO polypept
15	840	41.3	351	22	AAM38889	Human polypeptide
16	840	41.3	351	24	ABU71151	Human PRO864 prote
17	840	41.3	351	24	ABU65608	Human secreted/tra
18	840	41.3	351	24	ABU65941	Novel human secret
19	840	41.3	351	24	ABU67445	Human secreted/tra
20	840	41.3	351	24	ABU61105	Human PRO864 polyp
21	840	41.3	351	24	ABU65303	Human PRO polypept
22	840	41.3	351	24	ABU58439	Human PRO polypept
23	840	41.3	351	24	ABU55975	Human secreted/tra
24	840	41.3	351	24	ABU56970	Human PRO polypept
25	840	41.3	351	24	ARU10549	Human secreted/tra
26	840	41.3	365	22	AAM40675	Human polypeptide
27	840	41.3	365	22	AAE09707	Human gene 3 encod
28	836.5	41.1	352	23	AAU96847	Human NOV1b protei
29	834.5	41.0	352	23	AAU96846	Human Wnt-like pro
30	834	41.0	351	19	AAW86276	Signal transductio
31	834	41.0	351	24	AAE34075	WNT4 protein. Uni
32	834	41.0	351	24	ABU55886	Human WNT-4 prote
33	827.5	40.6	352	23	ABG60221	Human Wnt-like pro
34	827.5	40.6	352	23	ABG60222	Human Wnt-like pro
35	804	39.5	351	21	AAV57272	Wnt-4AF and Wnt-5c
36	787.5	38.7	365	21	AAV81693	Human Wnt-6 protei
37	787.5	38.7	365	22	AAB88439	Human membrane or
38	787.5	38.7	365	22	AAB49769	Amyloid-beta prote
39	787.5	38.7	365	24	ABU55888	Human WNT-6 prote
40	785	38.6	360	21	AAV70734	Human Wnt-2 protei
41	785	38.6	360	21	AAV57595	Human Wnt-2 protei
42	785	38.6	360	24	AAE34039	WNT-2 protein. Un
43	785	38.6	360	24	ABU55883	Human WNT-2 prote
44	766.5	37.6	365	21	AAV70739	Human Wnt-5a prote
45	766.5	37.6	365	21	AAV57600	Human Wnt-5a prote

ALIGNMENTS

RESULT 1

AAY56108

ID AAY56108 standard; Protein; 370 AA.

XX

AC AAY56108;

XX

DT 08-FEB-2000 (first entry)

XX

DE Human int-1 mammary oncogene protein sequence.

XX

KW Human; Wnt1; hWnt1; int-1; mammary oncogene; Alzheimer's disease;

KW Wingless 1; apoptosis.

XX

OS Homo sapiens.

XX

PN CA2200794-A.

XX

PD 24-SEP-1998.

XX

PF 24-MAR-1997; 97CA-2200794.

XX

PR 24-MAR-1997; 97CA-2200794.

XX

PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX

PI Fraser EE, St George-Hyslop PH;

XX

DE WPI; 1989-620995/54.

XX

DE N-PSDB; AAZ35965.

XX

PT Nucleic acids encoding the protein Wingless 1 which is involved in the development of Alzheimer's disease and may be used to identify and produce candidate therapeutic agents -

XX

PS Disclosure; Page -; 26pp; English.

XX

CC The present invention describes nucleic acids and proteins designated
CC Wingless 1 (wnt1), which are involved in the development of Alzheimer's
CC disease. The nucleic acids have a variety of uses for preventing,
CC diagnosing and treating Alzheimer's disease. For example, nucleic acids
CC (or vectors) encoding wnt1 may be administered to treat Alzheimer's
CC disease by rectifying mutations or deletions in a patient's genome that
CC affect the activity of wnt1 by expressing inactive proteins or to
CC supplement the patients own production of wnt1 polypeptides. Conversely,
CC antisense nucleic acid molecules may be administered to down regulate
CC wnt1 expression by binding with the cells own wnt1 genes and preventing
CC their expression. The nucleic acid probes and complementary sequences
CC may also be used as DNA probes in diagnostic assays (e.g. polymerase
CC chain reactions (PCR)) to detect and quantitate the presence of similar
CC nucleic acid sequences in samples, and hence which patients may be in
CC need of restorative therapy. They may also be used to study the
CC expression and function of wnt1 polypeptides and their role in the
CC pathology of Alzheimer's and in normal metabolism. Anti-wnt1 antibodies
CC and wnt1 antagonists may also be used to down regulate wnt1 expression
CC and activity and increase rates of apoptosis. The present sequence
CC represents the human int-1 mammary oncogene protein encoded by the
CC GENBANK accession # X03072 given in Z35965 from the present invention.

CC The present sequence is not given in the specification but is derived
CC from the GENBANK number given.

XX

SQ Sequence 370 AA;

Query Match 100.0%; Score 2036; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.2e-195;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60
Db      1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60

QY     61 LQLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
Db     61 LQLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120

QY    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180
Db    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180

QY    181 GREFVDSGEKGRDLRFLMNLHNNEAGR'TTVFSEMRQECKCHGMSGSC'TVRTCWMRLPTLR 240
Db    181 GREFVDSGEKGRDLRFLMNLHNNEAGR'TTVFSEMRQECKCHGMSGSC'TVRTCWMRLPTLR 240

QY    241 AVGDVLRDRFDGASRVLYGNRGSNRRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCT 300
Db    241 AVGDVLRDRFDGASRVLYGNRGSNRRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCT 300

QY    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360
Db    301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360

QY    361 THTRVLHECL 370
Db    361 THTRVLHECL 370
```

RESULT 2

AAY70733

ID AAY70733 standard; protein; 370 AA.

XX

AC AAY70733;

XX

DT 24-JUL-2000 (first entry)

XX

DE Human Wnt-1 protein.

XX

KW Human Wnt-1; Wnt antagonist; contraceptive; contraceptive vaccine;

KW oocyte development; female primate contraception; oocyte viability;

KW monoclonal antibody; Wnt signalling.

XX

OS Homo sapiens.

XX

PN WO200021555-A1.

XX

PD 20-APR-2000.

XX
PF 13-OCT-1999; 99WO-US23640.
XX
PR 15-OCT-1998; 98US-0104355.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI McMahon AP, Parr BA, Vaino S;
XX
DR WPI; 2000-317845/27.
XX
PT Contraceptive composition for inhibiting oocyte development in a female
ST primate comprises a Wnt polypeptide antagonist -
XX
PS Example 3; Page 23; 57pp; English.
XX
CC The patent discloses a method of female primate contraception comprising
CC administering an antagonist of a Wnt polypeptide, inhibiting oocyte
CC development. Wnt polypeptides are useful for promotive maturation of an
CC immature oocyte. Wnt polypeptides are also useful for increasing the
CC number of mature oocytes and to enhance oocyte viability. The present
CC sequence is the human Wnt-1 protein. Soluble fragments of Wnt
CC polypeptides have the ability to inhibit Wnt signalling, e.g., by
CC blocking binding of a naturally-occurring Wnt protein to its receptor.
CC They may be used to generate monoclonal antibodies which can inhibit
CC oocyte development.
XX
CC Sequence 370 AA;

Query Match 100.0%; Score 2036; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.2e-195;
Matched 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS	60
Db	1	MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS	60
QY	61	LQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG	120
Db	61	LQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG	120
QY	121	CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF	180
Db	121	CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF	180
QY	181	GREFVDSGEKGRDLRFLMNLHNEAGRTTVFSEMREQCKCHGMSGCTVRTCWMRLPTLR	240
Db	181	GREFVDSGEKGRDLRFLMNLHNEAGRTTVFSEMREQCKCHGMSGCTVRTCWMRLPTLR	240
QY	241	AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT	300
Db	241	AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLPEPDAHKPPSPHDLVYFEKSPNFCT	300
QY	301	YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRTVCNCTFHWCCCHVSCRNC	360
Db	301	YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRTVCNCTFHWCCCHVSCRNC	360

Qy 361 THTRVLHECL 370
| | | | | | | |
Db 361 THTRVLHECL 370

RESULT 3

AAAY57594

ID AAY57594 standard; Protein; 370 AA.

XX

AC AAY57594;

XX

DT 02-MAR-2000 (first entry)

XX

DE Human Wnt-1 protein.

XX

KW Wnt-1; neuronal growth; differentiation; regeneration;

KW dorsal neural progenitor cell; neurodegenerative disease;

KW Parkinson's disease; amyotrophic lateral sclerosis;

KW diffuse Lewy body disease; cortical-basal ganglionic degeneration;

KW Hallervorden-Spatz disease; myoclonic epilepsy.

XX

OS Homo sapiens.

XX

PN WO9957248-A1.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1998; 98WO-US08716.

XX

PR 30-APR-1998; 98WO-US08716.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI McMahon AP, Lee SK, Takada S;

XX

BR WPI; 2000-062145/05.

DR N-PSDB; AAZ47788.

XX

PT Enriched populations of mammalian neural precursor cells, for treating

PT Parkinson's disease -

XX

PS Claim 6; Page 4; 57pp; English.

XX

CC The present invention describes an enriched population of mammalian
CC neural precursor cells committed to a cell fate, the cells being
CC characterised in that they exhibit a stem cell phenotype in the presence
CC of a Wnt polypeptide but not in the absence of the Wnt polypeptide.

CC The enriched population of dopaminergic neuron precursor cells can be
CC used in a method for treating Parkinson's disease. The enriched
CC population of dorsal neural precursor cells can be used to induce

CC neuronal regeneration in an adult mammal suffering from a

CC neurodegenerative disorder. The disorder that can be treated is

CC Parkinson's disease, Amyotrophic lateral sclerosis, diffuse Lewy body

CC disease, cortical-basal ganglionic degeneration, Hallervorden-Spatz

CC disease or myoclonic epilepsy. The present sequence represents the

CC human Wnt-1 protein.

XX

SQ Sequence 370 AA;

Query Match 100.0%; Score 2036; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.2e-195;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGLWALLPGWVSATLLLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS 60

QY     61 LQLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQLLSRKQRRLLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG 120

QY    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLF 180

QY    181 GREFVDSGEKGRDLRFLMNLHNNEAGRITVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GREFVDSGEKGRDLRFLMNLHNNEAGRITVFSEMRQECKCHGMSGCTVRTCWMRLPTLR 240

QY    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCT 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCT 300

QY    301 YSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCTPHWCCHVSCRNC 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 YSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCTPHWCCHVSCRNC 360

QY    361 THTRVLHECL 370
      ||||||||
Db    361 THTRVLHECL 370
```

RESULT 4

AAE34038

ID AAE34038 standard; Protein; 370 AA.

XX

AC AAE34038;

XX

DT 02-MAY-2003 (first entry)

XX

DE WNT-1 protein.

XX

KW drug screening; toxicology assay; signalling pathway; WNT-1 protein.

XX

OS Unidentified.

XX

FN W0200290992-A2.

XX

PD 14-NOV-2002.

XX

PF 29-APR-2002; 2002WO-GB01946.

XX

PR 04-MAY-2001; 2001GB-0011004.

XX

Qy 301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNC 360

Qy 361 THTRVLHECL 370
 |||||||||
 Db 361 THTRVLHECL 370

RESULT 5

ABU55882

ID ABU55882 standard; Protein; 370 AA.

XX

AC ABU55882;

XX

DT 25-MAR-2003 (first entry)

XX

DE Human WNT-1 protein.

XX

KW Notch; Wnt; embryonic stem cell; embryogenesis; human;
 KW differentiation; ligand; Parkinson's disease; Huntington's disease;
 KW motor neuron disease; heart disease; diabetes; liver disease;
 KW cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200277294-A2.

XX

PD 03-OCT-2002.

XX

PE 25-MAR-2002; 2002WO-GB01195.

XX

PR 23-MAR-2001; 2001GB-0007296.

PR 23-MAR-2001; 2001GB-0007299.

PR 17-APR-2001; 2001GB-0009346.

XX

PA (AXOR-) AXORDIA LTD.

XX

PI Andrews P, Walsh J, Gokhale P;

XX

DR WPI; 2003-092852/08.

DR N-PSDB; ABX75310.

XX

PT Modulating the differentiation of embryonic stem cells by providing
 PT ligands which bind receptors in the Notch and Wnt pathways, useful for
 PT treating diseases such as Parkinson's, Huntington's, heart disease,
 PT diabetes and AIDS -

XX

PS Disclosure; Fig 31; 121pp; English.

XX

CC The invention relates to modulating the differentiation of an embryonic
 CC stem cell, comprising: (a) providing a culture of embryonic stem cells;
 CC (b) providing at least one ligand or its active binding fragment,
 CC capable of binding its cognate receptor polypeptide expressed by the
 CC embryonic stem cell; (c) forming a culture comprising embryonic stem
 CC cells and the ligand; and (d) growing the cell culture. Also included
 CC are: (1) Modulating the differentiation of embryonic stem cells,

CC comprising: (a) providing a cell transfected with a nucleic acid molecule
 CC selected from: (i) any of 9 fully defined Wnt nucleic acid sequences;
 CC (ii) a nucleic acid molecule that hybridises to the nucleic acid in
 CC (i), and which encodes a ligand capable of modulating embryonic stem
 CC cell differentiation, or capable of binding a Wnt receptor; or
 CC (iii) nucleic acid molecules which are degenerate as a result of the
 CC genetic code to the sequences of (i) or (ii); (b) forming a culture
 CC comprising the cell identified in (a) with an embryonic stem cell; and
 CC (c) growing the culture for the maintenance and/or differentiation of
 CC the embryonic stem cell; (2) Inhibiting the differentiation of embryonic
 CC stem cells, comprising: (a) providing at least one polypeptide or its
 CC active fragment, that are inhibitors of the Wnt signalling pathway;
 CC (b) forming a culture comprising the cell identified in (a) with an
 CC embryonic stem cell; and (c) growing the culture for the maintenance of
 CC embryonic stem cells in an undifferentiated state; or (3) Inhibiting the
 CC differentiation of embryonic stem cells, comprising: (a) providing a cell
 CC transfected with a nucleic acid molecule selected from: (i) a molecule
 CC encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises
 CC to the molecule of (i) and encodes a polypeptide capable of inhibiting
 CC Wnt signalling; and (iii) nucleic acid molecules which are degenerate as
 CC a result of the genetic code to the sequences of (i) or (ii); (b) forming
 CC a culture comprising the cell identified in (a) with an embryonic stem
 CC cell; and (c) growing the culture for the maintenance of embryonic stem
 CC cells in an undifferentiated state; and (4) A cell, therapeutic cell or
 CC cell culture obtainable by any of the methods cited above.
 CC The therapeutic cell of the present invention is useful in the
 CC treatment of an animal, preferably a human, comprising administering a
 CC cell composition comprising embryonic stem cells which have been
 CC induced to differentiate into at least one cell-type. The cell is also
 CC useful for the manufacture of a composition for use in treatment of
 CC diseases such as Parkinson's disease, Huntington's disease, motor
 CC neuron disease, heart disease, diabetes, liver disease (e.g.
 CC cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome).
 CC The present sequence is represents a Wnt or Notch pathway protein
 CC (i.e. a ligand for the method of the invention)

XX
 SQ Sequence 370 AA;

Query Match: 100.0%; Score 2036; DB 24; Length 370;
 Best Local Similarity 100.0%; Pred. No. 5.2e-195;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLWALLPGWVSATLLALLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS	60
Db	1	MGLWALLPGWVSATLLALLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPS	60
Qy	61	LQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG	120
Db	61	LQLLSRKQRRRLIRQNPGLHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRG	120
Qy	121	CRETAFIFAITSAGVTHSVAPSCSEGSIESCTDYRRRGPGGPDWHWGGCSDNIDFGRLF	180
Db	121	CRETAFIFAITSAGVTHSVAPSCSEGSIESCTDYRRRGPGGPDWHWGGCSDNIDFGRLF	180
Qy	181	GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCVTRTCWMRLPTLR	240
Db	181	GREFVDSGEKGRDLRFLMNLHNNEAGRTTVFSEMRQECKCHGMSGSCVTRTCWMRLPTLR	240

Qy 241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLLEPEDPAHKPPSPHDLVYFEKSPNFCT 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 AVGDVLRDRFDGASRVLYGNRGSNRASRAELLRLLEPEDPAHKPPSPHDLVYFEKSPNFCT 300

Qy 301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCCTFHWCCHVSCRNC 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 YSGRLGTAGTAGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCCTFHWCCHVSCRNC 360

Qy 361 THTRVLHECL 370
 |||||||||
 Db 361 THTRVLHECL 370

RESULT 6

AAB19785

ID AAB19786 standard; Protein; 370 AA.

XX

AC AAB19786;

XX

DT 19-FEB-2001 (first entry)

XX

DE Human Wnt-1 protein involved in kidney tubulogenesis.

XX

KW Wnt-1; human; kidney; tubulogenesis; chronic renal failure;

KW renal cell carcinoma; polycystic kidney disease;

KW chronic obstructive uropathy; virus-induced nephropathy;
 KW therapy.

OS Homo sapiens.

SI WO200061630-A1.

PD 19-OCT-2000.

XX

PF 08-APR-1999; 99WO-US07745.

XX

FR 08-APR-1999; 99WO-US07745.

XX

FA (HARD) HARVARD COLLEGE.

XX

PI McMahon AP, Kispert A, Vainio S;

XX

DR WPI; 2000-679466/66.

DR N-PSDB; AAA88884.

XX

PT Inducing kidney tubule formation in a post-natal mammal, involves
 PT administering a substantially pure Wnt polypeptide or its agonist

XX

PS Claim 18; Page 7-8; 53pp; English.

XX

CC The present sequence is that of human Wnt-1, a protein that acts as
 CC a trigger to start an intrinsic program in mesenchymal cells which
 CC leads to the formation of complex nephron-like structures. Kidney
 CC tubule formation in a post-natal mammal is stimulated by
 CC administering a Wnt polypeptide or a nucleic acid encoding it. The
 CC Wnt polypeptide is selected from Wnt-4 or a Wnt-1 class protein

Qy 250 FDGASRVLYGN-----RGSNRASRAELL----- 272
 ||||:| | || |:
 Db 265 FDGATRVQVTNSLRATNALAPVSPNAAGSNSVGSNGLIIPQSGLVYGEERMLNDHMPD 324
 Qy 273 -----RLEPEDPAHKPPSP 286
 :| | :| |||
 Db 325 ILLENSHPISKIHHNPMSPNSLPQAGQGRGRRGRQGRKHNRYPQLNPHNPEHKPPGS 384
 Qy 287 HDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCN 346
 |||| | ||:| | :| | || || || :| :||| |:|||||:| | |||
 Db 385 KDLVYLEPSPSFCEKNLRQGILGTHGRQCNETSLGVDGGLMCCGRGYRRDEVVVVERCA 444
 Qy 347 CTFHWCCHVSCRNCTHTRVLHECL 370
 ||||| | | :| | :||: ||
 Db 445 CTFHWCCEVKCKLCRTKKVIYTCL 468

RESULT 8

AA57596

ID AAY57596 standard; Protein; 352 AA.

XX

AC AAY57596;

XX

DE 02-MAR-2000 (first entry)

XX

DE Murine Wnt-3a protein.

XX

KW Wnt-1; neuronal growth; differentiation; regeneration;

KW dorsal neural progenitor cell; neurodegenerative disease;

KW Parkinson's disease; amyotrophic lateral sclerosis;

KW diffuse Lewy body disease; cortical-basal ganglionic degeneration;

KW Hallervorden-Spatz disease; myoclonic epilepsy.

XX

OS Mus sp.

XX

PN W09957248-A1.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1998; 98WO-US08716.

XX

PR 30-APR-1998; 98WO-US08716.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI McMahon AP, Lee SK, Takada S;

XX

DR WPI; 2000-062145/05.

DR

N-PSDB; AAZ47790.

XX

PT Enriched populations of mammalian neural precursor cells, for treating

PT Parkinson's disease -

XX

PS Claim 12; Page 5; 57pp; English.

XX

CC The present invention describes an enriched population of mammalian

CC neural precursor cells committed to a cell fate, the cells being

QY 94 KWQFRNRRWNCPTAPGP-HLFGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCT 152
 : ||| |||| | :|| :::: ||:||: || |||| :| |||:||: |
 Db 81 QHQFRGRRWNCTTIDSLAIFGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICG 140

QY 153 CDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGRDLRFLMNLHNEAGRITTVFS 212
 || :|| | | ||||:: || | || | || |||||:|
 Db 141 CDSHHKGPPGEGWKWGGCSEDADFGVLVSREFADARENRPDARSAMNKHNEAGRITILD 200

QY 213 EMRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDLRDRFDGASRVLYGNRGSNRASRAELL 272
 | :|||>||| |:|| | ||:|| :||:| || :: :| || :
 Db 201 HMHLKCKCHGLSGSCEVKTCWWAQPDFRAIGDFLKDKYDSASEMVV---EKHRESRGWVE 257

QY 273 RLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTAGRACNSSSPALDGCCELLCCGR 332
 | : |||: ||||:| |||| : |:|| | || :| :|||:|||||
 Db 258 TLRKYSLFKPPTERDLVYYENSPNFCEPNPETGSFGTRDRTCNVTSHGIDGCDLLCCGR 317

QY 333 GHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
 || |||:: |:|| ||||:|||: | :| |
 Db 318 GHNTRTEKRKEKCHCIFHWCCYVSCQECIRIYDVHTC 354

RESULT 10

AA41719

ID AAY41719 standard; Protein; 351 AA.

XX

AC AAY41719;

XX

DE 07-DEC-1999 (first entry)

XX

DE Human PRO864 protein sequence.

XX

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.

XX

OS Homo sapiens.

XX

PN WO9946281-A2.

XX

PD 16-SEP-1999.

XX

DE 08-MAR-1999; 99WO-US05028.

XX

PR 10-MAR-1998; 98US-0077450.

PR 11-MAR-1998; 98US-0077632.

PR 11-MAR-1998; 98US-0077641.

PR 11-MAR-1998; 98US-0077649.

PR 12-MAR-1998; 98US-0077791.

PR 13-MAR-1998; 98US-0078004.

PR 17-MAR-1998; 98US-0040220.

PR 20-MAR-1998; 98US-0078886.

PR 20-MAR-1998; 98US-0078910.

PR 20-MAR-1998; 98US-0078936.

PR 20-MAR-1998; 98US-0078939.

PR 25-MAR-1998; 98US-0079294.

PR 26-MAR-1998; 98US-0079656.

PR	27-MAR-1998;	98US-0079663.
PR	27-MAR-1998;	98US-0079664.
PR	27-MAR-1998;	98US-0079689.
PR	27-MAR-1998;	98US-0079728.
PR	27-MAR-1998;	98US-0079786.
PR	30-MAR-1998;	98US-0079920.
PR	30-MAR-1998;	98US-0079923.
PR	31-MAR-1998;	98US-0080105.
PR	31-MAR-1998;	98US-0080107.
PR	31-MAR-1998;	98US-0080165.
PR	31-MAR-1998;	98US-0080194.
PR	01-APR-1998;	98US-0080327.
PR	01-APR-1998;	98US-0080328.
PR	01-APR-1998;	98US-0080333.
PR	01-APR-1998;	98US-0080334.
PR	08-APR-1998;	98US-0081049.
PR	08-APR-1998;	98US-0081070.
PR	08-APR-1998;	98US-0081071.
PR	09-APR-1998;	98US-0081195.
PR	09-APR-1998;	98US-0081203.
PR	09-APR-1998;	98US-0081229.
PR	15-APR-1998;	98US-0081817.
PR	15-APR-1998;	98US-0081838.
PR	15-APR-1998;	98US-0081952.
PR	15-APR-1998;	98US-0081955.
PR	21-APR-1998;	98US-0082568.
PR	21-APR-1998;	98US-0082569.
PR	22-APR-1998;	98US-0082700.
PR	22-APR-1998;	98US-0082704.
PR	22-APR-1998;	98US-0082804.
PR	23-APR-1998;	98US-0082767.
PR	23-APR-1998;	98US-0082796.
PR	27-APR-1998;	98US-0083336.
PR	28-APR-1998;	98US-0083322.
PR	29-APR-1998;	98US-0083392.
PR	29-APR-1998;	98US-0083495.
PR	29-APR-1998;	98US-0083496.
PR	29-APR-1998;	98US-0083499.
PR	29-APR-1998;	98US-0083500.
PR	29-APR-1998;	98US-0083545.
PR	29-APR-1998;	98US-0083554.
PR	29-APR-1998;	98US-0083558.
PR	29-APR-1998;	98US-0083559.
PR	30-APR-1998;	98US-0083742.
PR	05-MAY-1998;	98US-0084366.
PR	06-MAY-1998;	98US-0084414.
PR	06-MAY-1998;	98US-0084441.
PR	07-MAY-1998;	98US-0084598.
PR	07-MAY-1998;	98US-0084600.
PR	07-MAY-1998;	98US-0084627.
PR	07-MAY-1998;	98US-0084637.
PR	07-MAY-1998;	98US-0084639.
PR	07-MAY-1998;	98US-0084640.
PR	07-MAY-1998;	98US-0084643.
PR	13-MAY-1998;	98US-0085323.
PR	13-MAY-1998;	98US-0085338.
PR	13-MAY-1998;	98US-0085339.

Qy 134 GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGR- 192
 || :| |:| | :| | | :| | | | | :| | :| | | : :
 Db 119 GVAFVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKG 178

Qy 193 --DLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDLRDRF 250
 | | | | | | | | : : | | | | | : | | | | : | | | | : : : |
 Db 179 ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKF 238

Qy 251 DGASRVLYGNRGSNRASRAELLRLPEDEPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310
 ||| : | | : | | : | | : | | | | | : | | | | |
 Db 239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT 291

Qy 311 AGRACNSSSPALDGCELLCCGPGHRTTRQVTERCNCNTHFWCCHVSCRCNCTHTRVLHEC 369
 || | | : | | : | | | | | | | | : | | | | | | | | | |
 Db 292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCCKFHWCCFVKCRQCQRLVELHTC 350

RESULT 11

AAB44275

ID AAB44275 standard; Protein; 351 AA.

XX

AC AAB44275;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human PRO664 (UNQ426) protein sequence SEQ ID NO:226.

XX

CT Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;

EN expressed sequence tag; detection; cancer.

XX

OS Homo sapiens.

ZX

PN W0000053756-A2.

XX

PD 14-SEP-2000.

XX

PF 18-FEB-2000; 2000WO-US04341.

XX

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

```

XX      (GETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI      Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI      Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI      Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI      Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR      WPI; 2000-611443/58.
DR      N-PSDB; AAC78505.
XX
PT      Novel PRO polypeptides and polynucleotides used in detection methods,
PT      to target bioactive molecules to specific cells, and to modulate
PT      cellular activities -
XX
PS      Claim 12; Fig 83; 636pp; English.
XX
CC      AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC      sequence tag) sequences which encode secreted or transmembrane PRO
CC      polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC      activity. The polynucleotides and polypeptides can be used for detecting
CC      the presence of PRO polypeptides in samples, for linking bioactive
CC      molecules to cells and for modulating biological activities of cells,
CC      using the polypeptides for specific targeting. The polypeptide targeting
CC      can be used to kill the target cells, e.g. for the treatment of cancers.
CC      The polypeptide pairs provide specific targeting of bioactive molecules
CC      to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC      the isolation of the PRO polynucleotide sequences.
XX
SQ      Sequence 351 AA;

Query Match          41.3%; Score 840; DB 21; Length 351;
Best Local Similarity 44.8%; Pred. No. 2.6e-75;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

Qy      14 TLLALAAALPAALAAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLLIR 73
       :| | : | : :| | : | | : : : : : | : | :| : :
Db      9 SLRLLVFAVFSAAASN-----WLYLAKLSSVSGSISEETCE-----KLKGLIQRQVMCK 58

Qy      74 QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133
       :| : : || | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      59 RNLEVMSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVTQGTREAAFYVAISSA 118

Qy      134 GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGRLFGREFVDSGEKGR- 192
       || :| :| :| | :| | || | : | | | | | :| | : || | : :
Db      119 GVAFVAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKG 178

Qy      193 --DLRFLMNLHNNEAGRRTTVFSEMRQECKCHGMSGSCVTVRTCWMRLPTLRAVGDVLRDRF 250
       | | | | | | | | | : : | | | | | :| | | | :| | | | :| :|
Db      179 ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKF 238

Qy      251 DGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310
       ||| : | || :| | | | : | | : | | | | | | | | | | | |
Db      239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT 291

Qy      311 AGRACNSSSPALDGCCELLCCGRGHRTRTQRVTERCNCFTFWCCHVSCRNCTHTRVLHEC 369

```

Db

292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTC 350

RESULT 12

AA57270

ID AAY57270 standard; Protein; 351 AA.

XX

AC AAY57270;

XX

DT 06-JUN-2000 (first entry)

XX

DE Wnt-4AF and Wnt-5c homolog polypeptide #1.

XX

KW Wnt; Wnt-4AF; Wnt-5C; frizzled gene; membrane protein; diagnostic;
therapeutic; human.

XX

OS Homo sapiens.

XX

PN WO200012117-A1.

XX

PD 09-MAR-2000.

XX

PF 20-AUG-1993; 99WO-US19046.

XX

PR 31-AUG-1998; 98US-0098440.

PR 31-AUG-1998; 98US-0098453.

PR 30-OCT-1998; 98US-0106462.

PR 09-DEC-1998; 98US-0111588.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Edmonds BT, Su W;

XX

DR WPI; 2000-256491/22.

DR N-PSDB; AAZ90451.

XX

PT New gene encoding the Wnt-4AF and Wnt-5C homolog polypeptide involved
in developmental control during embryonic development is useful to
diagnose and treat related disease

XX

PS Claim 9; Page 72-73; 41pp; English.

XX

CC The invention provides isolated nucleic acid sequences (AAZ90451-454)
encoding Wnt-4AF and Wnt-5C homolog polypeptides (AAY57270-273). The
polypeptides can be expressed by standard recombinant methodology. They
upregulate gene expression by binding to Frizzled class of membrane
proteins The Wnt antibodies can be used in diagnostics and therapeutics,
while chimeric and transgenic animals can provide models of disease for
testing the effectiveness of therapeutic or diagnostic agents.

XX

SQ Sequence 351 AA;

Query Match 41.3%; Score 840; DB 21; Length 351;

Best Local Similarity 44.8%; Pred. No. 2.6e-75;

Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

SQ Sequence 351 AA;

Query Match 41.3%; Score 840; DB 21; Length 351;
Best Local Similarity 44.8%; Pred. No. 2.6e-75;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY	14	TLLLLAALPAALAAANSSGRWWGI VNVASSTNLLTDSKSLQLVLEPSLQLSRKQRRLLIR	73
Db	9	SLRLLVFAVFSAAASN-----WLYLAKLSSVGSISEETCE-----KLKGLIQRQVQMCK	58
QY	74	QNP GILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS A	133
Db	59	RNLEVMDSVRRGAQIAL EECQYQFRNRRWNCSTLDSL P VFGKVVTQGTREAAFVYAISSA	118
QY	134	GVTHSVARSCSEGSIESCTCDYRRRGPGGPDWHWGGCSDNIDFGR LFGREFVDSGEKGR-	192
Db	119	GVAFAVTRACSSGELEKCGCDRTVHGVS PQGFQWSGCSDNIAYGVAFSQS FVDVRERSKG	178
QY	193	--DLRFLMNLHNNEAGR TTVFSEMRQECKCHGMSG SCTVRTCWMRLPTLRAGDVL RDRF	250
Db	179	ASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAPV PFRQVGHALKEKF	238
QY	251	DGASRVLYGNRGSNRASRAELLRLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT	310
Db	239	DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT	291
QY	311	AGRACNSSSPALDGC ELLCCGRGHRTRTQRVTERC NCTFHWCCHVSCRNCTHTRVLHEC	369
Db	292	RGRTC NKTSKAIDGCELLCCGRGFHTAQVELAERC SCKFHWCCFVKRCQCQRLVELHTC	350

DT 18-DEC-2001 (first entry)

XX
DE Human PRO polypeptide sequence #40.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
PA (GETH) GENENTECH INC.

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

DR WPI: 2001-602746/68.

 ΣX

P.T.

 λX

XX

CC

:CC

CC

cc

200

55

cc

CC

60

1

Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

100

•

10

•••

10

Db

292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFWCCFVKCRQCQRLVELHTC 350

RESULT 15

AAM38889

ID AAM38889 standard; Protein; 351 AA.

XX

AC AAM38889;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2034.

XX

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PP 26-DEC-2000; 2000WC-US34263.

XX

PP 21-JAN-2000; 2000US-0488725.

PP 25-APR-2000; 2000US-0552317.

PP 09-JUL-2000; 2000US-0598042.

PP 19-JUL-2000; 2000US-0620312.

PP 03-AUG-2000; 2000US-0653450.

PP 14-SEP-2000; 2000US-0662191.

PP 19-OCT-2000; 2000US-0693036.

PP 29-NOV-2000; 2000US-0727344.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX

DR WPI; 2001-442253/47.

DR N-PSDB; AAI58045.

XX

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX

PS Example 3; SEQ ID NO 2034; 10078pp; English.

XX

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX

SQ Sequence 351 AA;

Query Match 41.3%; Score 840; DB 22; Length 351;
 Best Local Similarity 44.8%; Pred. No. 2.6e-75;
 Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

```

Qy      14 TLLALAALPAALAANSSGRWWGIVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRRLIR 73
      :| | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      9 SLRLLVFAVFSAAASN-----WLYLAKLSSVGSISEEETCE-----KLKGLIQRQVQMCK 58

Qy      74 QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPGPHLFGKIVNRGCRETAFIFAITS 133
      :| :| :| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      59 RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPLVFGKVVITQGTREAAAFVYAISS 118

Qy     134 GVTHSVARSCSEGSIESCTCDYRRRGPGPDWHWGGCSDNIDFGRLFGREFVDSSEKGR- 192
      || :| | :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     119 GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFEVDVRERSKG 178

Qy     193 --DLRFLMNLHNNEACRTTVFSEMRQECKCHGMSGCTVRTCWMRLPTLRAVGDVLRDRF 250
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     179 ASSSPALMNLHNNEACRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKF 238

Qy     251 DGASKVLYGNRGSNRAELRLLEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGT 310
      ||| : | | | : | | | | | | | | | | | | | | | | | | | | | |
Db     239 DGATEVEPRRVGSSRA-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGT 291

Qy     311 AGRACNSSSPALDGCELLCCGRGHRTRTQRVTERCNCTFHWCCHVSCRNCTHTRVLHEC 369
      || | | : | | : | | | | | | | | | | | | | | | | | | | | | |
Db     292 RGRTCNKTSKAIDGCELLCCGRGFHTAQVELAERCCKFHWCCFVKCRQCQRLVELHTC 350

```

Search completed: January 21, 2004, 10:46:46
 Job time : 46 secs